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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:32:26 ; Search time 308.446 Seconds
(without alignments)
479.804 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

Sequence: 1 cuggauagcuggaucacacccuug 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3 AAC64407	AAC64407 Human Nog
2	25	100.0	75	9 ACC81049	ACC81049 Human Nog
3	25	100.0	75	9 ACC81057	ACC81057 Human Nog
4	25	100.0	90	9 ACC81058	ACC81058 Human Nog
5	25	100.0	105	9 ACC81059	ACC81059 Human Nog
6	25	100.0	120	9 ACC81054	ACC81054 Human Nog
7	25	100.0	198	9 ACC81055	ACC81055 Human Nog
8	25	100.0	198	9 ACC81056	ACC81056 Human Nog
9	25	100.0	198	12 ADQ16424	ADQ16424 Nucleotid
10	25	100.0	198	12 ADRI1367	ADRI1367 Human Nog
11	25	100.0	261	2 AAV23697	AAV23697 Human NSP
12	25	100.0	404	2 AAX41193	AAX41193 Human sec
13	25	100.0	600	4 AAF90323	AAF90323 Human NOG
14	25	100.0	639	6 ABN96987	ABN96987 Gene #348
15	25	100.0	668	6 ABN86601	ABN86601 Human pol
16	25	100.0	770	3 AAV72983	AAV72983 Human NSP
17	25	100.0	799	2 AAV23695	AAV23695 Human NSP
18	25	100.0	991	2 AAX97587	AAX97587 Extended
19	25	100.0	994	12 ADPI18854	ADPI18854 Human sec
20	25	100.0	1122	3 AAZ56888	AAZ56888 Human MAG

C 21	25	100.0	1122	4 AAF90325	AAF90325 Human NOG
C 22	25	100.0	1213	2 AAX04379	AAX04379 Human sec
C 23	25	100.0	1216	6 ABA05903	ABA05903 Human RTN
C 24	25	100.0	1514	6 ABK34580	ABK34580 Human CDN
C 25	25	100.0	1599	10 ADI62860	ADI62860 Human apo
C 26	25	100.0	1610	3 AAZ36230	AAZ36230 cDNA enco
C 27	25	100.0	1683	4 AAD08386	AAD08386 Human sec
C 28	25	100.0	1694	4 AAK94408	AAK94408 Human ful
C 29	25	100.0	1694	12 ADL31137	ADL31137 Full leng
C 30	25	100.0	1758	4 AAF32725	AAF32725 Human sec
C 31	25	100.0	1785	12 ADK14166	ADK14166 Human aut
C 32	25	100.0	1798	6 ABK90135	ABK90135 DNA enco
C 33	25	100.0	1980	4 AAI98079	AAI98079 Human neu
C 34	25	100.0	2052	6 ABK90133	ABK90133 DNA enco
C 35	25	100.0	2235	6 ABV94681	ABV94681 Human pan
C 36	25	100.0	2240	3 AAC64406	AAC64406 Human Nog
C 37	25	100.0	2386	2 AAV30920	AAV30920 Human sec
C 38	25	100.0	2386	5 AAF98399	AAF98399 Human CDN
C 39	25	100.0	2610	11 ADI31056	ADI31056 Human CDN
C 40	25	100.0	2934	12 ADQ16433	ADQ16433 Construct
C 41	25	100.0	3579	3 AAZ56886	AAZ56886 Human MAG
C 42	25	100.0	3579	4 AAF90324	AAF90324 Human NOG
C 43	25	100.0	3579	6 ABK90134	ABK90134 DNA enco
C 44	25	100.0	3579	6 ABN86601	ABN86601 Human neu
C 45	25	100.0	3579	12 ADO07886	ADO07886 Human pol

ALIGNMENTS

RESULT 1

AAC64407
ID AAC64407 standard; RNA; 25 BP.

XX AAC64407;

DT 08-FEB-2001 (first entry)

XX Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:3.

XX Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
XX stress-phosphorylated endoplasmic reticulum protein; cytosstatic;
XX gene therapy; cell growth; cellular stress response; neuron growth;
XX regulator of oxidative stress; inhibitor of neurite outgrowth;
XX axon regeneration; diagnosis; cancer; identification; antisense;
XX phosphorothioate; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..25

FT /*tag= a
/note= "phosphorothioate linkages"

FT WO2000060083-A1.

XX 12-OCT-2000.

XX 07-APR-2000; 2000WO-US009383.

XX 08-APR-1999; 99US-0128372P.

XX 21-JUN-1999; 99US-0140331P.

XX (CHIR) CHIRON CORP.

XX Wei D, Halenbeck R, Williams LT;

XX WPI; 2000-665007/64.

XX Novel protein associated with cell stress response useful for modulating
XX stress levels, cell growth, diagnosis and treatment of cancer and
XX malignant growth and for identifying agonists and antagonists.

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic
CC reticulum protein, designated Nogo B. Nogo B has cytostatic activity and
CC is a modulator of the storage and exchange of calcium, cell growth and
CC cellular stress response. It can: regulate oxidative stress; inhibit
CC neurite outgrowth, neuron growth and axon regeneration. Nogo B
CC polypeptides and polynucleotides are useful for modulating stress levels
CC and cellular stress-response, cell growth and viability, diagnosis and
CC treatment of cancer, malignant growth and other Nogo B related diseases.
CC Nogo B polypeptides are also useful to screen combinatorial libraries to
CC identify agonist or antagonist. Antibodies against Nogo B polypeptides
CC are useful for affinity chromatography and distinguishing Nogo B
CC polypeptides. The present sequence represents a human Nogo B
CC phosphorothioate antisense oligonucleotide from the present invention

XX
SQ Sequence 25 BP; 5 A; 7 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 1 CUGGAUAGCUUGGAUCACACCCUUG 25

RESULT 2
ACC81049/c
ID ACC81049 standard; cDNA; 75 BP.

XX
AC ACC81049;

DT 22-JUL-2003 (first entry)

XX
DE Human Nogo receptor inhibitor Pepl cDNA.

XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;
KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
KW demyelinating disease; multiple sclerosis; monophasic demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1..75
FT /*tag= a
FT /product= "Human Nogo receptor inhibitor Pepl"
FT /note= "No start/stop codon given"

XX
PN WO2003031462-A2.

XX 17-APR-2003.

XX 04-OCT-2002; 2002WO-US032007.

XX 06-OCT-2001; 2001US-00972599.

XX (UYA) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.

DR P-PSDB; ABR59668.

XX New human Nogo receptor polypeptides and nucleic acids, useful for
PT decreasing inhibition of axonal growth by a central nervous system
PT neuron, or in treating central nervous system disease, disorder or
PT injury, e.g. spinal cord injury.

XX
PS Disclosure; Page 135; 148pp; English.

XX The invention relates to a novel nucleic acid encoding a polypeptide
CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
CC human Nogo receptor (Ngr) NTLRRCT domain), or residues 27-309 of P1 with
CC 1-20 conservative amino acid substitutions, and less than a complete CTS
CC domain, provided that a partial CTS domain, if present, consists of no
CC more than the first 39 consecutive residues. The polynucleotide may have a use
CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
CC axonal growth by a central nervous system (CNS) neuron. The Ngr
CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-
CC dependent signal transduction in the central nervous system neuron may be
CC used in treating central nervous system disease, disorder or injury, e.g.
CC spinal cord injury. Expression of an Ngr protein may be associated with
CC inhibition of axonal regeneration following cranial, cerebral or spinal
CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
CC monophasic demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
CC sequence is used in the exemplification of the invention

XX
SQ Sequence 75 BP; 25 A; 15 C; 18 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 75;
Best Local Similarity 72.0%; Pred. No. 0.068;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 36 CTGGTAGCTTGGATCACACCTTG 12

RESULT 3
ACC81057/c
ID ACC81057 standard; cDNA; 75 BP.

XX
AC ACC81057;

DT 22-JUL-2003 (first entry)

XX Human NogoA partial gene #2.

XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;
KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
KW demyelinating disease; multiple sclerosis; monophasic demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1..75
FT /*tag= a
FT /product= "Partial human NogoA"
FT /note= "No start/stop codon given"

XX
PN WO2003031462-A2.

XX 17-APR-2003.

XX 04-OCT-2002; 2002WO-US032007.

XX 06-OCT-2001; 2001US-00972599.

XX (UYA) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.

DR P-PSDB; ABR59676.

XX New human Nogo receptor polypeptides and nucleic acids, useful for
PT decreasing inhibition of axonal growth by a central nervous system

PT neuron, or in treating central nervous system disease, disorder or
 PT injury, e.g. spinal cord injury.

PS Disclosure; Page 139; 148pp; English.

CC The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The nucleic acid of the
 CC invention has neuroprotective activity. The polynucleotide may have a use
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
 CC axonal growth by a central nervous system (CNS) neuron. The NGR
 CC polypeptide or an agent inhibits the binding of Nogo to NGR or NGR-
 CC dependent signal transduction in the central nervous system neuron may be
 CC used in treating central nervous system disease, disorder or injury, e.g.
 CC spinal cord injury. Expression of an NGR protein may be associated with
 CC inhibition of axonal regeneration following cranial, cerebral or spinal
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
 CC monophasic demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
 CC sequence is used in the exemplification of the invention

XX Sequence 75 BP; 25 A; 16 C; 18 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 75;
 Best Local Similarity 72.0%; Pred. No. 0.068;
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGAUCACACCCUUG 25
 Db 33 CTGGATAGCTTGGATCACCCTTG 9

RESULT 4
 ACC81058/c

ID ACC81058 standard; cDNA; 90 BP.

XX ACC81058;

XX 22-JUL-2003 (first entry)

XX Human NogoA partial gene #3.

XX Human; Nogo receptor; NGR; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
 KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..90

FT /*tag= a
 FT /product= "Partial human NogoA"
 FT /note= "No start/stop codon given"

XX WO2003031462-A2.

XX 17-APR-2003.

XX 04-OCT-2002; 2002WO-US032007.

XX 06-OCT-2001; 2001US-00972599.

XX (UYUA) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.

DR P-PSDB; ABR59677.

XX New human Nogo receptor polypeptides and nucleic acids, useful for
 PT decreasing inhibition of axonal growth by a central nervous system
 PT neuron, or in treating central nervous system disease, disorder or
 PT injury, e.g. spinal cord injury.

XX Disclosure; Page 140; 148pp; English.

XX The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The nucleic acid of the
 CC invention has neuroprotective activity. The polynucleotide may have a use
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
 CC axonal growth by a central nervous system (CNS) neuron. The NGR
 CC polypeptide or an agent inhibits the binding of Nogo to NGR or NGR-
 CC dependent signal transduction in the central nervous system neuron may be
 CC used in treating central nervous system disease, disorder or injury, e.g.
 CC spinal cord injury. Expression of an NGR protein may be associated with
 CC inhibition of axonal regeneration following cranial, cerebral or spinal
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
 CC monophasic demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
 CC sequence is used in the exemplification of the invention

XX Sequence 90 BP; 29 A; 18 C; 21 G; 22 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 90;

Best Local Similarity 72.0%; Pred. No. 0.07;

Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGAUCACACCCUUG 25

Db 33 CTGGATAGCTTGGATCACCCTTG 9

RESULT 5

ACC81059/c

ID ACC81059 standard; cDNA; 105 BP.

XX ACC81059;

XX 22-JUL-2003 (first entry)

XX Human NogoA partial gene #4.

XX Human; Nogo receptor; NGR; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
 KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..105

FT /*tag= a
 FT /product= "Partial human NogoA"
 FT /note= "No start/stop codon given"

XX WO2003031462-A2.

XX 17-APR-2003.

XX 04-OCT-2002; 2002WO-US032007.

XX 06-OCT-2001; 2001US-00972599.

XX (UYUA) UNIV YALE.

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XX Strittmatter SM;
XX WPI; 2003-393433/37.
XX P-PSDB; ABR59678.
XX New human Nogo receptor polypeptides and nucleic acids, useful for
XX decreasing inhibition of axonal growth by a central nervous system
XX neuron, or in treating central nervous system disease, disorder or
XX injury, e.g. spinal cord injury.
XX Disclosure; Page 140; 148pp; English.
XX The invention relates to a novel nucleic acid encoding a polypeptide
XX comprising amino acid residues 27-309 of a 473 amino acid sequence (PI,
XX human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of PI with
XX 1-20 conservative amino acid substitutions, and less than a complete CTS
XX domain, provided that a partial CTS domain, if present, consists of no
XX more than the first 39 consecutive residues. The nucleic acid of the
XX invention has neuroprotective activity. The polynucleotide may have a use
XX in gene therapy. The nucleic acid is useful for decreasing inhibition of
XX axonal growth by a central nervous system (CNS) neuron. The Ngr
XX polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-
XX dependent signal transduction in the central nervous system neuron may be
XX used in treating central nervous system disease, disorder or injury, e.g.
XX spinal cord injury. Expression of an Ngr protein may be associated with
XX inhibition of axonal regeneration following cranial, cerebral or spinal
XX trauma, stroke or a demyelinating disease, such as multiple sclerosis,
XX monophasic demyelination, encephalomyelitis, multifocal
XX leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
XX sequence is used in the exemplification of the invention
XX
XX Sequence 105 BP; 32 A; 19 C; 28 G; 26 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 9; Length 105;
Best Local Similarity 72.0%; Pred. No. 0.072;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTGGATCACCCTTG 9
RESULT 6
ACC81054/c
ID ACC81054 standard; cDNA; 120 BP.
XX ACC81054;
XX
XX 22-JUL-2003 (first entry)
XX Human Nogo receptor inhibitor Pep2-41 cDNA.
XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;
XX axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
XX cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
XX demyelinating disease; multiple sclerosis; monophasic demyelination;
XX encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
XX ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..120
XX /*tag= a
XX /product= "Human Nogo receptor inhibitor Pep2-41"
XX /note= "No start/stop codon given"
XX
XX WO2003031462-A2.
XX 17-APR-2003.
XX
XX 04-OCT-2002; 2002WO-US032007.
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XX 06-OCT-2001; 2001US-00972599.
XX (UYVA ) UNIV YALE.
XX Strittmatter SM;
XX WPI; 2003-393433/37.
XX P-PSDB; ABR59673.
XX New human Nogo receptor polypeptides and nucleic acids, useful for
XX decreasing inhibition of axonal growth by a central nervous system
XX neuron, or in treating central nervous system disease, disorder or
XX injury, e.g. spinal cord injury.
XX Disclosure; Page 137; 148pp; English.
XX The invention relates to a novel nucleic acid encoding a polypeptide
XX comprising amino acid residues 27-309 of a 473 amino acid sequence (PI,
XX human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of PI with
XX 1-20 conservative amino acid substitutions, and less than a complete CTS
XX domain, provided that a partial CTS domain, if present, consists of no
XX more than the first 39 consecutive residues. The nucleic acid of the
XX invention has neuroprotective activity. The polynucleotide may have a use
XX in gene therapy. The nucleic acid is useful for decreasing inhibition of
XX axonal growth by a central nervous system (CNS) neuron. The Ngr
XX polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-
XX dependent signal transduction in the central nervous system neuron may be
XX used in treating central nervous system disease, disorder or injury, e.g.
XX spinal cord injury. Expression of an Ngr protein may be associated with
XX inhibition of axonal regeneration following cranial, cerebral or spinal
XX trauma, stroke or a demyelinating disease, such as multiple sclerosis,
XX leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
XX sequence is used in the exemplification of the invention
XX
XX Sequence 120 BP; 38 A; 21 C; 30 G; 31 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 9; Length 120;
Best Local Similarity 72.0%; Pred. No. 0.073;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTGGATCACCCTTG 9
RESULT 7
ACC81055/c
ID ACC81055 standard; DNA; 198 BP.
XX ACC81055;
XX
XX 22-JUL-2003 (first entry)
XX Human Nogo receptor binding region DNA.
XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;
XX axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
XX cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
XX demyelinating disease; multiple sclerosis; monophasic demyelination;
XX encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
XX ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..198
XX /*tag= a
XX /product= "Human Nogo receptor binding region"
XX /note= "No start/stop codon given"
XX
XX WO2003031462-A2.
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XX PD 24-JUN-2004.
XX PF
XX PF 05-DEC-2003; 2003WO-GB005323.
XX PR
XX PR 06-DEC-2002; 2002US-0431620P.
XX PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
XX PA (DENI/) DENISON C M.
XX PI
XX PI Xiao Z;
XX DR
XX DR WPI; 2004-468811/44.
XX DR P-PSDB; ADQ16419.
XX PT
XX PT New peptides that interact with myelin proteins Nogo, TNF and MAG, useful
XX PT in preparing a composition for treating CNS damage, spinal cord injury or
XX PT stroke.
XX PS
XX PS Disclosure; SEQ ID NO 16; 81pp; English.
XX CC
XX CC The present sequence encodes Nogo-66 domain b. The specification
XX CC describes peptides which interact with the myelin proteins Nogo
XX CC (specifically the Nogo-66 domain), the extracellular matrix glycoprotein
XX CC tenascin-R (TN-R) (specifically TN-R epidermal growth factor like (TNR-
XX CC EGFL)) and myelin-associated glycoprotein (MAG). These proteins have
XX CC neural growth inhibitory activity. The peptide is isolated from a 7-mer
XX CC phage display library exposed to a plate coated with the target protein.
XX CC Peptides of the invention are useful in preparing a composition for
XX CC treating central nervous system (CNS) damage, spinal cord injury or
XX CC stroke. The peptides may also be used in vaccines against myelin
XX CC antigens. The vaccine is based on the specific inhibitory portions of
XX CC major myelin proteins, instead of the whole protein.
XX SQ
XX SQ Sequence 198 BP; 56 A; 36 C; 49 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.079;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
DB 33 CTGGATAGCTTGGATCACCCTTG 9

RESULT 10
ADRI13967/c
ID ADRI13967 standard; cDNA; 198 BP.
XX AC
XX AC ADRI13967;
XX DT
XX DT 23-SEP-2004 (first entry)
XX DE
XX DE Human Nogo-66 cDNA.
XX KW
XX KW ss; gene; human; myelin-associated glycoprotein; MAG; neural growth;
XX KW neural regeneration; apoptosis; amyotrophic lateral sclerosis;
XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX KW multiple sclerosis; Creutzfeldt-Jacob disease; kuru;
XX KW multiple system atrophy; Lou Gehrig's disease;
XX KW progressive supranuclear palsy.
XX OS
XX OS Homo sapiens.
XX FH
XX FH Key Location/Qualifiers
XX FT CDS 1..198
XX FT /*tag= a
XX FT /partial
XX FT /product= "Nogo-66"
XX FT /note= "No start and stop codons given"
XX FT
XX FN
XX FN US2004121341-A1.
XX XX

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PD 24-JUN-2004.
XX PF
XX PF 20-DEC-2002; 2002US-00327213.
XX PR
XX PR 20-DEC-2002; 2002US-00327213.
XX PA (FILB/) FILBIN M T.
XX PA (DOME/) DOMENICONI M.
XX PA (CAOZ/) CAO Z.
XX PI
XX PI Filbin MT, Domeniconi M, Cao Z;
XX DR
XX DR WPI; 2004-479666/45.
XX DR P-PSDB; ADRI13968.
XX PT
XX PT New myelin-associated glycoprotein (MAG) derivative comprises a mutation
XX PT in or flanking MAG Ig-like domain 5 (IgD5), excluding the MAG derivative
XX PT MAG (DI-3)-Fc, useful promoting neural growth and regeneration.
XX PS
XX PS Disclosure; SEQ ID NO 10; 81pp; English.
XX CC
XX CC The invention relates to a myelin-associated glycoprotein (MAG)
XX CC derivative comprising a mutation in or flanking MAG Ig-like domain 5
XX CC (IgD5), excluding the MAG derivative MAG (DI-3)-Fc, where the mutation
XX CC reduces or eliminates the ability of the derivative to regulate neurite
XX CC outgrowth as compared to endogenous or soluble MAG without eliminating
XX CC binding to neuronal surfaces. The inhibitors of MAG are useful for
XX CC promoting neural growth and regeneration. They are also useful for
XX CC treating neural degeneration associated with injuries, disorders, or
XX CC diseases. The disorder, disease, or condition is associated with
XX CC apoptosis or results from a demyelinating disease and includes
XX CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
XX CC Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease,
XX CC kuru, multiple system atrophy, amyotrophic lateral sclerosis (Lou
XX CC Gehrig's disease), or progressive supranuclear palsy. The present
XX CC sequence represents the human Nogo-66 cDNA.
XX SQ
XX SQ Sequence 198 BP; 56 A; 36 C; 49 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.079;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
DB 33 CTGGATAGCTTGGATCACCCTTG 9

RESULT 11
AAV23697/c
ID AAV23697 standard; cDNA; 261 BP.
XX AC
XX AC AAV23697;
XX DT
XX DT 24-JUL-1998 (first entry)
XX DE
XX DE Human NSPLP protein coding sequence fragment.
XX KW
XX KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;
XX KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO9806841-A2.
XX FT
XX FT 19-FEB-1998.
XX PF
XX PF 24-JUL-1997; 97WO-US013469.
XX PR
XX PR 12-AUG-1996; 96US-00700607.
XX PA
XX PA (INCY-) INCYTE PHARM INC.
XX XX

```

PI Bandman O, Au-Young J, Goli SK, Hillman J;
 DR WPI; 1998-159533/14.
 XX Human neuro-endocrine-specific protein-like proteins - useful for
 PT diagnosis, monitoring and treatment of cancer and neuro-degenerative
 PT disease.
 XX
 PS Disclosure; Page 45; 73pp; English.
 XX
 CC This sequence encodes a human neuroendocrine-specific protein-like
 CC protein (NSPLP) of the invention. Recombinant cells transformed with the
 CC DNA are used to express the NSPLP proteins, which are used to treat
 CC cancer and neurodegenerative diseases such as amyotrophic lateral
 CC sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be
 CC used to inhibit activity of the NSPLP proteins. Antibodies specific for
 CC NSPLP are used for diagnosis and monitoring treatment of diseases
 CC associated with NSPLP expression, in usual immunoassays, and to isolate
 CC NSPLP from natural sources. The NSPLP proteins, or their fragments can
 CC also be used in drug screening to identify NSPLP antagonists. The nucleic
 CC acid can be used diagnostically and for monitoring treatment (in
 CC hybridisation or amplification assays); to isolate closely related
 CC sequences; in gene therapy for both sense and antisense applications
 CC (including use of ribozymes) and for mapping the natural genomic sequence
 XX
 SQ Sequence 261 BP; 62 A; 59 C; 56 G; 67 T; 0 U; 17 Other;
 Query Match 100.0%; Score 25; DB 2; Length 261;
 Best Local Similarity 72.0%; Pred. No. 0.082;
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUGGAUAGCUUGGAUACACACCCUUG 25
 Db 124 CTGGATAGCTTGGATCACCACCCCTTG 100
 RESULT 12
 AAX41193/c
 ID AAX41193 standard; cDNA; 404 BP.
 AC AAX41193;
 XX
 DT 17-JUN-1999 (first entry)
 DE Human secreted protein 5' EST SEQ ID NO:137.
 XX
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulation; haematopoiesis regulation; tissue growth regulation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO9906548-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-IB001222.
 XX
 PR 01-AUG-1997; 97US-00905135.
 XX
 PA (GEST) GENSET.
 XX
 FI Dumas Milne Edwards J, Duclert A, Lacroix B;
 XX
 DR WPI; 1999-153778/13.
 DR P-PSDB; AAY12360.
 XX
 PT New nucleic acids encoding human secreted proteins - obtained from cDNA
 PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,
 PT umbilical cord, placenta and colon tissue.

XX
 PS Claim 1; Page 319; 824pp; English.
 XX
 CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY12261 to
 CC AAY12514, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell
 XX
 SQ Sequence 404 BP; 110 A; 75 C; 108 G; 111 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 2; Length 404;
 Best Local Similarity 72.0%; Pred. No. 0.088;
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUGGAUAGCUUGGAUACACACCCUUG 25
 Db 347 CTGGATAGCTTGGATCACCACCCCTTG 323
 RESULT 13
 AAF90323/c
 ID AAF90323 standard; cDNA; 600 BP.
 XX
 AC AAF90323;
 XX
 DT 23-JUL-2001 (first entry)
 DE Human NOGO-C cDNA.
 XX
 KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;
 KW neuroprotective; nontropic; neuroleptic; antiparkinsonian;
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200136631-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 14-NOV-2000; 2000WO-GB004345.
 XX
 PR 15-NOV-1999; 99GB-00026995.
 PR 24-JAN-2000; 2000GB-00001550.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 FI Michalovich D, Prinjha R;
 XX
 DR WPI; 2001-343822/36.
 DR P-PSDB; AAB82348.
 XX
 PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
 PT gene and may be useful in the treatment of neural disorders including
 PT Alzheimer's and Parkinson's diseases.
 XX
 PS Claim 1; Page 25; 25pp; English.
 XX
 CC The present sequence is that of cDNA encoding human NOGO-C (see

CC AAB2348). NOGO-C is a novel splice variant of the human NOGO gene on
CC chromosome 2p21. 2 Other splice variants, NOGO-A and NOGO-B, have
CC previously been identified. The invention provides NOGO-C polypeptides
CC and polynucleotides, and methods for producing such polypeptides by
CC recombinant techniques. Also disclosed are methods for utilising NOGO-C
CC polypeptides and polynucleotides in the treatment of diseases including
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular
CC disorders, psychiatric disorders and developmental disorders. Also
CC provided are methods for identifying agonists and agonists for use in
CC treating conditions associated with NOGO-C imbalance, and diagnostic
CC assays for detecting diseases associated with inappropriate NOGO-C
CC activity or levels
XX
SQ Sequence 600 BP; 161 A; 113 C; 144 G; 182 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 4; Length 600;
Best Local Similarity 72.0%; Pred. No. 0.093;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 216 CTGGATAGCTGGATCACCCTTG 192
RESULT 14
ABL96987/c
ID ABL96987 standard; DNA; 639 BP.
XX
AC ABL96987;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #3485 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
FN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030589.
XX
PR 02-OCT-2000; 2000US-0237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer, hepatocellular
PT carcinoma or metastatic liver tumor in a patient, involves detecting the
PT level of expression of two or more genes in a liver tissue sample.
XX
PS Claim 1; SEQ ID NO 3485; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumor in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data

CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 639 BP; 138 A; 114 C; 149 G; 147 T; 0 U; 91 Other;
Query Match 100.0%; Score 25; DB 6; Length 639;
Best Local Similarity 72.0%; Pred. No. 0.094;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 415 CTGGATAGCTGGATCACCCTTG 391
RESULT 15
ABL9601/c
ID ABL9601 standard; cDNA; 668 BP.
XX
AC ABL9601;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 163.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
XX
PR 19-MAY-2000; 2000US-0205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR P-PSDB; ABB89192.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
PS Claim 4; SEQ ID NO 163; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

Search completed: July 30, 2005, 12:18:05
Job time : 309.446 secs

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C 3	25	100.0	198	6	CQ827995	CQ827995 Sequence
C 4	25	100.0	198	6	AX195263	AX195263 Sequence
C 5	25	100.0	261	6	AR028534	AR028534 Sequence
C 6	25	100.0	404	6	BD076183	BD076183 5' EST of
C 7	25	100.0	600	9	HS4251385	HS4251385 Homo sapi
C 8	25	100.0	639	6	AX410838	AX410838 Sequence
C 9	25	100.0	799	6	AR028522	AR028522 Sequence
C 10	25	100.0	994	6	BD139293	BD139293 Extended
C 11	25	100.0	1079	9	BC007109	BC007109 Homo sapi
C 12	25	100.0	1122	6	BD249448	BD249448 Protein s
C 13	25	100.0	1122	9	HS4251384	HS4251384 Homo sapi
C 14	25	100.0	1151	9	BC001035	BC001035 Homo sapi
C 15	25	100.0	1213	6	BD194907	BD194907 86 human
C 16	25	100.0	1213	6	CQ855235	CQ855235 Sequence
C 17	25	100.0	1466	9	BC071848	BC071848 Homo sapi
C 18	25	100.0	1485	9	BC010737	BC010737 Homo sapi
C 19	25	100.0	1525	9	AX130812	AX130812 Homo sapi

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REFERENCE
AUTHORS      Strittmatter,S.M.
TITLE        Nogo receptor-mediated blockade of axonal growth
JOURNAL      Patent: WO 0151520-A 17 19-JUL-2001;
              YALE UNIVERSITY (US)
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Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 3
LOCUS      CQ827995      198 bp      DNA      linear      PAT 05-JUL-2004
DEFINITION Sequence 16 from Patent WO2004052922.
ACCESSION  CQ827995
VERSION     CQ827995.1 GI:49731526
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS     Xiao,Z.C.
TITLE       Peptides, antibodies thereto, and their use in the treatment of
            central nervous system damage
JOURNAL     Patent: WO 2004052922-A 16 24-JUN-2004;
            Singapore General Hospital Pty. Ltd. (SG)
FEATURES
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              /db_xref="taxon:9606"

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Best Local Similarity 72.0%; Pred. No. 0.14;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 4
LOCUS      AX195263      198 bp      DNA      linear      PAT 28-AUG-2001
DEFINITION Sequence 19 from Patent WO0151520.
ACCESSION  AX195263
VERSION     AX195263.1 GI:15385816
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS     Strittmatter,S.M.
TITLE       Nogo receptor-mediated blockade of axonal growth
JOURNAL     Patent: WO 0151520-A 19 19-JUL-2001;
            YALE UNIVERSITY (US)
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source       Location/Qualifiers
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HVNCTIKELRRLFLVDVDSL"

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Best Local Similarity 72.0%; Pred. No. 0.14;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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Db 36 CTGGATAGCTTGGATCACACCCCTTG 12

RESULT 5
LOCUS      AR028524      261 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5858708.
ACCESSION  AR028524
VERSION     AR028524.1 GI:5940497
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
            1 (bases 1 to 261)
            Bandman,O., Au-Young,J., Goli,S.K. and Hillman,J.L.
            Polynucleotides encoding two novel human neuroendocrine-specific
            proteins
            Patent: US 5858708-A 9 12-JAN-1999;
            Location/Qualifiers
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              /mol_type="unassigned DNA"

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Best Local Similarity 72.0%; Pred. No. 0.14;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 124 CTGGATAGCTTGGATCACACCCCTTG 100

RESULT 6
LOCUS      BD076183      404 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 5' EST of tissue-nonspecific secretory protein.
ACCESSION  BD076183
VERSION     BD076183.1 GI:22621786
KEYWORDS    JP 2001512011-A/131.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 404)
            Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
            5' EST of tissue-nonspecific secretory protein
            Patent: JP 2001512011-A 131 21-AUG-2001;
            GENSET
            OS Homo sapiens (human)
            PN JP 2001512011-A/131
            PD 21-AUG-2001
            PF 31-JUL-1998 JP 2000505289
            PR 01-AUG-1997 US 08/905135
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QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
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Db 216 CTGGATAGCTTGGATCACACCCCTTG 192

RESULT 8
AX410838/c
LOCUS AX410838 639 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 3485 from Patent WO0229103.
ACCESSION AX410838
VERSION AX410838.1 GI:21443543
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3485 11-APR-2002;
GENE LOGIC INC (US)
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Db 415 CTGGATAGCTTGGATCACACCCCTTG 391

RESULT 9
AR028522/c
LOCUS AR028522 799 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5858708.
ACCESSION AR028522
VERSION AR028522.1 GI:5940495
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Bandman,O., Au-Young,J., Goli,S.K. and Hillman,J.I.
TITLE Polynucleotides encoding two novel human neuroendocrine-specific
proteins
JOURNAL Patent: US 5858708-A 2 12-JAN-1999;
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RESULT 10
BD139293/c
LOCUS BD139293 994 bp DNA linear PAT 18-SEP-2002
DEFINITION Extended cDNA of secretory protein.
ACCESSION BD139293

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VERSION BDI39293.1 GI:23234238
KEYWORDS JP 2002508182-A/45.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
TITLE Extended cDNA of secretory protein
JOURNAL Patent: JP 2002508182-A 45 19-MAR-2002;
GENSET
OS Homo sapiens (human)
PN JP 2002508182-A/45
PD 19-MAR-2002
PF 17-DEC-1998 JP 2000539136
PR 17-DEC-1997 US 60/069957, 09-FEB-1998 US 60/074121 PR
13-APR-1998 US 60/081563, 10-AUG-1998 US 60/096116 PI LYDIE
BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
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C12N1/21,
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Von Heijne matrix
CC score 8.6
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Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
BC007109/c
LOCUS BC007109 1079 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens reticulon 4, transcript variant 3, mRNA (CDNA clone
IMAGE:4291127), complete cds.
ACCESSION BC007109
VERSION BC007109.1 GI:13937989
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Udwin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Iqbal,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

```


REMARK COMMENT	<p>Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA</p> <p>NIH-MGC Project URL: http://mgc.nci.nih.gov</p> <p>On Aug 19, 2003 this sequence version replaced gi:12654418.</p> <p>Contact: MGC help desk</p> <p>Email: cgabbs-r@mail.nih.gov</p> <p>Tissue Procurement: ATCC</p> <p>cDNA Library Preparation: Rubin Laboratory</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</p> <p>DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;</p> <p>Web site: http://www.nisc.nih.gov/</p> <p>Contact: nisc_mgc@nhgri.nih.gov</p> <p>Akhter, N., Ayèle, K., Beckström-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Skatripp, S., Thomas, P.J., Touchman, J.W., Tsoung, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.</p>
-------------------	--

Clone distribution: WCC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 4 Row: c Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5902015
This clone has the following problem: The cds is short compared to the longest cds in the locus.

FEATURES
SOURCE

gene

CDS

ORIGIN

```
Query Match      100.0%; Score 25; DB 9; Length 1151;
Best Local Similarity 72.0%; Pred. No. 0.15;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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1 CTGGAAAGCTTGGCAUCACACCCCTUG 25

401 CTGGATAGCTTGGATCACAACCTTG 377

RESULT 15

BD194907/c	BD194907	1213 bp	DNA	linear	PAT 17-JUL-2003
LOCUS					
DEFINITION	86 human secreted proteins.				

FEATURES	source
HERZEGOVINA	
Location/Qualifiers	
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ORIGIN

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Query Match      100.0%; Score 25; DB 9; Length 1122;
Best Local Similarity 72.0%; Pred. No. 0.15;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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1 CUGGAUAGCUUGGAUCACACCCUUG 25

db 738 CTGGATAGCTTGGATCACACCCCTTG 714

RESULT 14

BC001035/c	BC001035	1151 bp	linear	PRI 29-JUN-2004
LOCUS			mRNA	
DEFINITION	Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone IMAGE:3139770), complete cds.			

ACCESSION	BC001033
VERSION	BC001035.2
	GI:33875905

NETWORKS
SOURCE
Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1151)

1 (bases 1 to 1151)

Mammalia; Eutheria; Primates; Cacerinini; Homiidae; Homo.

1 (bases 1 to 1151)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heltón, E., Kettelman, M., Maman, A., Rodríguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodríguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED
12477932

REFERENCE 2 (bases 1 to 10)

AUTHORS **Strausberg, R.**

TITLE
Direct Submission
Submitted (17-NOV-2000) National Institutes of Health, Mammalian
JOURNAL

Search completed: July 30, 2005, 12:54:23
Job time: 732.757 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:50:11 ; Search time 2561.15 Seconds
(without alignments)
371.555 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

Sequence: 1 cuggaagcunggaucacaccuug 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	25	100.0	176	2	AW897156 CM0-NN005
C 3	25	100.0	201	2	BE169952 CM0-HT053
C 4	25	100.0	243	6	CD216746 EST S52 H
C 5	25	100.0	257	1	AA371486 EST83278
C 6	25	100.0	274	2	BS080807 QV1-BT063
C 7	25	100.0	280	7	CF125576 UI-HF-EL0
C 8	25	100.0	286	5	BU073029 im29a06.Y
C 9	25	100.0	288	5	B0311462 QV4-BN009
C 10	25	100.0	297	6	C14200 C14200 Clon
C 11	25	100.0	310	2	BF173127 MYR0856a
C 12	25	100.0	327	7	CN429721 170006000
C 13	25	100.0	328	1	AA303835 EST16527
C 14	25	100.0	342	6	CD706840 EST23367
C 15	25	100.0	346	2	BE007854 QV0-BN014
C 16	25	100.0	350	2	BE763621 QV2-NT004
C 17	25	100.0	353	7	R96423 YG37F03.r1
C 18	25	100.0	374	1	AV725869 AV725869
C 19	25	100.0	381	1	AA341035 EST46634
C 20	25	100.0	386	7	T81226 YG25A06.r1
C 21	25	100.0	388	1	AA100508 zn51c07.r
C 22	25	100.0	388	1	AA192599 zq01f08.r
C 23	25	100.0	395	1	AV729281 AV729281
C 24	25	100.0	396	1	AA307342 EST178236

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C 26	25	100.0	400	4	BG620263	BG620263 602618547
C 27	25	100.0	410	1	AU297299	AU297299 AU297299
C 28	25	100.0	413	5	BX497982	BX497982 DFEZp779M
C 29	25	100.0	416	1	AA088462	AA088462 z182b09.r
C 30	25	100.0	417	4	BM826161	BM826161 K-EST0098
C 31	25	100.0	417	7	N55351	N55351 YV47d08.s1
C 32	25	100.0	418	2	BE694253	BE694253 QV2-BT068
C 33	25	100.0	423	6	C15922	C15922 C15922 Clon
C 34	25	100.0	428	6	CA389096	CA389096 c906c09.Y
C 35	25	100.0	436	2	BE080786	BE080786 QV1-BT063
C 36	25	100.0	439	4	BM504391	BM504391 ih22b12.Y
C 37	25	100.0	440	7	CR558096	CR558096 DFEZp459M
C 38	25	100.0	440	7	N31239	N31239 YX53f07.r1
C 39	25	100.0	448	7	W68688	W68688 zd35e02.s1
C 40	25	100.0	448	7	W68781	W68781 zd35e02.r1
C 41	25	100.0	450	2	BF671862	BF671862 602151760
C 42	25	100.0	457	2	AW995369	AW995369 QV0-BN004
C 43	25	100.0	457	7	T71810	T71810 YC62e07.r1
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C 45	25	100.0	460	6	CB147989	CB147989 K-EST0204

ALIGNMENTS

RESULT 1
CB295964/c
LOCUS
DEFINITION
220010 rev_1_G08_r_056.abl Chimpanzee brain library Koos Pan
troglodytes_cDNA clone 220010 rev_1_G08_r_056.abl 5' similar to
human RTN4 neuroendocrine-specific protein C like (foccen), mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

FEATURES
source

CB295964 147 bp mRNA linear EST 28-FEB-2003
220010 rev_1_G08_r_056.abl Chimpanzee brain library Koos Pan
troglodytes_cDNA clone 220010 rev_1_G08_r_056.abl 5' similar to
human RTN4 neuroendocrine-specific protein C like (foccen), mRNA
sequence.
CB295964
CB295964.1 GI:28621394
EST.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
Hallmann, I., Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and
Paabo, S.
Selection on human genes as revealed by comparisons to chimpanzee
cDNA
Genome Res. (2003) In press
Contact: Paabo S
Evolutionary Genetics
Max-Planck-Institute for evolutionary Anthropology
Deutscher Platz 6, 04103 Leipzig, Germany
Tel: +49- (0)-341-3550 500
Fax: +49- (0)-341-3550 555
Email: paabo@eva.mpg.de
Seq primer: M13 reverse.
Location/Qualifiers
1. 147
/organism="Pan troglodytes"
/mol_type="mRNA"
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/sex="male"
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/clone_lib="Chimpanzee brain library Koos"
/note="Vector: pUchi; Site 1: Sfil-A, Site 2: Sfil-B; The
library was prepared using the SMART cDNA library
construction kit (Clontech), doing only primer extension,
but not PCR amplification of the cDNA. The only deviation
from the published protocol was that we cloned the cDNA
into a plasmid vector."

ORIGIN

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

TO THE
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ORIGIN

oy

RESULT 5

KEYWORDS

REFERENCE

TITLE

PUB

ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 280;
Best Local Similarity 72.0%; Pred. No. 0.64;
Matches 18; Conservative 7; Mismatches 0; Indels

Qy	1	CUGGAUAGCUUGGAUCACACCCUUG	25
		: : : : : : : : : : : : :	
Db	78	CTGGATAGCTTGGATCACACCCCTTG	54

RESULT 8
BU073029/c

LOCUS BU073029
DEFINITION im29a06.y1 Human insuli

sequ 5' s

ACCESSION BU073029
VERSION BU073029.1
KEYWORDS FST

KEYWORDS
SOURCE
ORGANISM

ORGANISM

REFERENCE
AUTHORS

AUTHORS

TITLE
JOURNAL

COMMENT

FEATURES

ORIGIN

**Best Local
Matches**

	EST. SOURCE ORGANISM	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	REFERENCE AUTHORS	1 (bases 1 to 297) Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Negata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiyah,H., Takaichi,A., Takeda,S., Watanabe,T., Takahaashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y. Fujiwara et al. (1995)
	TITLE JOURNAL COMMENT	Contacted: Teutomu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co.,Ltd 463-10 Kagasuno Kawachi-cho, Tokushima, Tokushima, 771-01 Japan Tel: 0886-65-2888 Fax: 0886-37-1035.
	FEATURES Source	Location/Qualifiers 1..297 /morganism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="GEN-O37D12" /clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
	ORIGIN	Query Match 100.0%; Score 25; DB 6; Length 297; Best Local Similarity 72.0%; Pred.No. 0.64; Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY		1 CUGGAUAGCUUGGUAUCACACCCTTG 25 :: ::: :: :: : DB 163 CTGGATAGCTTCGCATCACCCCTTG 139
	RESULT 11 BF173127/c LOCUS DEFINITION	BF173127 310 bp mRNA linear EST 23-MAR-2001 MYE0856a Myeloma (MYE) cDNA library Homo sapiens cdNA, mRNA sequence. BF173127 BF173127.1 GI:13439413
	ACCESSION VERSION KEYWORDS SOURCE	1 (bases 1 to 310) Claudio,J.O., Magih-Khan,E., Tang,H., Goncalves,J., Vorallia,M., Li,Z.H., Nadeem,V., Kukerman,E., Francisco-Pabalan,O., Liew,C.C., Woodgett,J.R. and Stewart,A.K. A molecular compendium of genes expressed in multiple myeloma Blood 100 (6), 2175-2186 (2002) 22188429 12200383
	JOURNAL MEDLINE PUBMED COMMENT	Contact: A. Keith Stewart, M.D. Oncology Research University Health Network 610 University Ave., S-126, Toronto, Ontario, MSG 2M9, Canada Tel: (416) 946-4639 Fax: (416) 946-6546 Email: k.stewart@utoronto.ca PCR Primers FORWARD: 5'-GCCAAGCTCGAAATTAA CCTCAACTTAAGGG-3' BACKWARD: 5'-CCAGTGAATTGTATAAGCCTCATCTATAGGGCG-3' Seq primer: 5'-GAAATTAA CCCTCACTTAAGG-3'.
	FEATURES Source	Location/Qualifiers 1..310 /morganism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /sex="male"

RESULT 13
AA303835/c
LOCUS
DEFINITION
AA303835 328 bp mRNA linear EST 18-APR-1997
EST16527 Aorta endothelial cells, TNF alpha-treated Homo sapiens
cDNA 5' end similar to similar to neuroendocrine-specific protein
C, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AA303835
AA303835.1 GI:1956187
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 328)

Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Hominidae.

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palances, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

JOURNAL MEDLINE PUBMED	COMMENT
<p> Rates up (1995) Nucleoside sequence bases 377 (6547 Suppl), 3-174 (1995) 96026280 7566098 Other_ESTs: THC181855 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 </p>	

ORIGIN	Query Match
/organism="Homo sapiens" /mol_type="mRNA" /db_xref="ATCC (inhost):115452" /db_xref="taxon:9606" /cell_type="endothelial cell" /dev_stage="adult" /clome.lib="Aorta endothelial cells, TNF alpha-treated" /note="Organ: aorta; Vector: pBluescript SK-; Site_1: ECORI; Site_2: XhoI"	100.0%; Score 25; DB 1; Length 328

Query Match	100.0%;	Score 25;	DB 1;	Length 328;
Best Local Similarity	72.0%;	Pred. No. 0.65;		

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:52:26 ; Search time 90.2027 Seconds
(without alignments)
453.500 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

Sequence: 1 cuggauagcuggaucacacccuug 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	25	100.0	261	2	US-08-700-607-9
c 2	25	100.0	601	4	US-09-949-016-117588
c 3	25	100.0	601	4	US-09-949-016-117589
c 4	25	100.0	799	2	US-08-700-607-2
c 5	25	100.0	1669	4	US-09-949-016-3253
c 6	25	100.0	2610	4	US-09-023-655-382
c 7	25	100.0	4822	3	US-09-484-970B-106
c 8	25	100.0	42075	4	US-09-949-016-14995
c 9	18.6	74.4	175236	4	US-09-949-016-14353
c 10	18.2	72.8	601	4	US-09-949-016-167886
c 11	18.2	72.8	1593	3	US-09-676-610B-25
c 12	18.2	72.8	1868	1	US-08-658-883B-1
c 13	18.2	72.8	1868	3	US-09-676-610B-26
c 14	18.2	72.8	3633	2	US-09-715-249-1
c 15	18.2	72.8	5532	2	US-08-475-035-3
c 16	18.2	72.8	5532	3	US-09-676-610B-17
c 17	18.2	72.8	63000	4	US-09-780-172-18
c 18	18.2	72.8	63926	4	US-09-949-016-16473
c 19	18.2	72.8	64626	4	US-09-949-016-12011
c 20	18.2	72.8	169998	3	US-09-676-610B-24
c 21	18.2	72.8	197496	4	US-09-877-177A-10
c 22	17.8	71.2	403	4	US-09-513-999C-1468
c 23	17.8	71.2	601	4	US-09-949-016-91585
c 24	17.8	71.2	601	4	US-09-949-016-91586
c 25	17.8	71.2	57837	4	US-09-949-016-14371
c 26	17.8	71.2	57839	4	US-09-949-016-17601
c 27	17.6	70.4	1227	4	US-09-710-279-2285

c 28	17.6	70.4	1557	3	US-09-134-001C-1907	Sequence 1307, Ap
c 29	17.6	70.4	3046	4	US-09-710-279-3782	Sequence 3782, Ap
c 30	17	68.0	226	4	US-09-621-376-16264	Sequence 16264, A
c 31	17	68.0	375	4	US-09-902-540-8294	Sequence 8294, Ap
c 32	17	68.0	601	4	US-09-949-016-25253	Sequence 25253, A
c 33	17	68.0	601	4	US-09-949-016-25254	Sequence 25254, A
c 34	17	68.0	601	4	US-09-949-016-26285	Sequence 26285, A
c 35	17	68.0	601	4	US-09-949-016-26286	Sequence 26286, A
c 36	17	68.0	601	4	US-09-949-016-26287	Sequence 26287, A
c 37	17	68.0	601	4	US-09-949-016-31105	Sequence 31105, A
c 38	17	68.0	601	4	US-09-949-016-31106	Sequence 31106, A
c 39	17	68.0	601	4	US-09-949-016-82471	Sequence 82471, A
c 40	17	68.0	601	4	US-09-949-016-116493	Sequence 116493, A
c 41	17	68.0	601	4	US-09-949-016-116511	Sequence 116511, A
c 42	17	68.0	601	4	US-09-949-016-124120	Sequence 124120, A
c 43	17	68.0	601	4	US-09-949-016-124121	Sequence 124121, A
c 44	17	68.0	601	4	US-09-949-016-142012	Sequence 142012, A
c 45	17	68.0	601	4	US-09-949-016-142013	Sequence 142013, A

ALIGNMENTS

RESULT 1
US-08-700-607-9/c
; Sequence 9, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: SPLNFET01
; CLONE: 28742

US-08-700-607-9
Query Match 100.0%; Score 25; DB 2; Length 261;
Best Local Similarity 72.0%; Pred. No. 0.015;
Matches 18; Conservative 0; Indels 0; Gaps 0;
Qy 1 CUGGAUAGCUGGAUACACCCUUG 25


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; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253

Query Match      100.0%; Score 25; DB 4; Length 1669;
Best Local Similarity 72.0%; Pred. No. 0.02;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
   |||:||||:||||:||||:||||:|
Db 430 CTGGATAGCTTGGATCACACCCCTTG 406

RESULT 6
US-09-023-655-382/c
; Sequence 382, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT14
; CLONE: 1508778
US-09-023-655-382

Query Match      100.0%; Score 25; DB 4; Length 2610;
Best Local Similarity 72.0%; Pred. No. 0.022;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
   |||:||||:||||:||||:||||:|
Db 1494 CTGGATAGCTTGGATCACACCCCTTG 1470

RESULT 7

US-09-484-970B-106/c
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 106
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match      100.0%; Score 25; DB 3; Length 4822;
Best Local Similarity 72.0%; Pred. No. 0.024;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
   |||:||||:||||:||||:||||:|
Db 3450 CTGGATAGCTTGGATCACACCCCTTG 3426

RESULT 8
US-09-949-016-14995/c
; Sequence 14995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14995
; LENGTH: 42075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14995

Query Match      100.0%; Score 25; DB 4; Length 42075;
Best Local Similarity 72.0%; Pred. No. 0.034;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
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Db 24830 CTGGATAGCTTGGATCACACCCCTTG 24806

RESULT 9
US-09-949-016-14353
; Sequence 14353, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
```

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14353
; LENGTH: 175236
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14353

Query Match      74.4%; Score 18.6; DB 4; Length 175236;
Best Local Similarity 64.0%; Pred. No. 51;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGAUCACACCCUUG 25
Db 132015 CTGGATAGCTGGATCAGGCGATG 132039

RESULT 10
US-09-949-016-167886/c
; Sequence 167886, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 167886
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-167886

Query Match      72.8%; Score 18.2; DB 4; Length 601;
Best Local Similarity 69.6%; Pred. No. 33;
Matches 16; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGAUAGCUUGAUCACACCCUUG 25
Db 599 GGAGAGCTAGGATCACCATTG 577

RESULT 11
US-09-676-610B-25/c
; Sequence 25, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
```

```
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 25
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)...(1462)
US-09-676-610B-25

Query Match      72.8%; Score 18.2; DB 3; Length 1593;
Best Local Similarity 65.2%; Pred. No. 39;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGAUAGCUUGAUCACACCCUUG 25
Db 828 GGACAGCTGGATCACCATTG 806

RESULT 12
US-08-658-983B-1/c
; Sequence 1, Application US/08658883B
; Patent No. 5708156
; GENERAL INFORMATION:
; APPLICANT: Ilekis, John V.
; TITLE OF INVENTION: An Epidermal Growth Factor
; RECEPTOR-LIKE GENE PRODUCT AND ITS USES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John V. Ilekis
; STREET: 4206 Linden Avenue
; CITY: Western Springs
; STATE: IL
; COUNTRY: U.S.A
; ZIP: 60558
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft DOS 6.2
; SOFTWARE: Microsoft No. 5708156epad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,883B
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5708156 Applicable
; FILING DATE: No. 5708156 Applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5708156 Applicable
; REGISTRATION NUMBER: No. 5708156 Applicable
; REFERENCE/DOCKET NUMBER: No. 5708156 Applicable
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-996-6273/708-246-9085
; TELEFAX: No. 5708156 Applicable
; TELE: No. 5708156 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1868 bases
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Term Placenta
; IMMEDIATE SOURCE:
; LIBRARY: cDNA
; FEATURE:
; OTHER INFORMATION: Deduced amino acid length
; of 381. Putative signal peptide Met-1 to Ala-24.
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US-08-658-883B-1

Query Match 72.8%; Score 18.2; DB 1; Length 1868;
Best Local Similarity 65.2%; Pred. No. 39;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGAUAGCUUGGAUCACACCCUUG 25
Db 1087 GGACAGCTTGGATCACACTTTG 1065
|||||:|||||:|

RESULT 13

US-09-676-610B-26/c
; Sequence 26, Application US/09676610B
; Patent No. 6444465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676.610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 26
; LENGTH: 1868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (504)...(1721)
US-09-676-610B-26

Query Match 72.8%; Score 18.2; DB 3; Length 1868;
Best Local Similarity 65.2%; Pred. No. 39;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGAUAGCUUGGAUCACACCCUUG 25
Db 1087 GGACAGCTTGGATCACACTTTG 1065
|||||:|||||:|

RESULT 14

US-09-715-249-1/c
; Sequence 1, Application US/09715249
; Patent No. 6790614
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS AG
; APPLICANT: VERES, GABOR
; APPLICANT: PIPPIG, SUSANNE
; TITLE OF INVENTION: selectable cell surface marker genes
; FILE REFERENCE: 4-31192
; CURRENT APPLICATION NUMBER: US/09/715.249
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: us 60/166594
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: us 09/539248
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: EGFR
US-09-715-249-1

Query Match 72.8%; Score 18.2; DB 4; Length 3633;
Best Local Similarity 65.2%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGAUAGCUUGGAUCACACCCUUG 25
Db 584 GGACAGCTTGGATCACACTTTG 562
|||||:|||||:|

RESULT 15

US-08-475-035-3/c
; Sequence 3, Application US/08475035
; Patent No. 5985553
; GENERAL INFORMATION:
; APPLICANT: KING, C. R.
; APPLICANT: KRAUS, MATTHIAS H.
; APPLICANT: AARONSON, STUART A.
; TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
; TITLE OF INVENTION: EGF RECEPTOR GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,035
; FILING DATE: 7 Jun 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.656
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3816
US-08-475-035-3

Query Match 72.8%; Score 18.2; DB 2; Length 5532;
Best Local Similarity 65.2%; Pred. No. 47;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGAUAGCUUGGAUCACACCCUUG 25
Db 770 GGACAGCTTGGATCACACTTTG 748
|||||:|||||:|

Search completed: July 30, 2005, 15:05:35
Job time : 91.2027 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:00:21 ; Search time 731.757 Seconds
(without alignment)
1655.441 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25
Sequence: 1 caacucaggaucagaugccc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20.8	83.2	182405	10	AC124978	AC124978 Mus muscu
2	20.8	83.2	230629	10	AC127332	AC127332 Mus muscu
3	20.8	81.6	27745	9	AF065393	AF065393 Homo sapi
4	20.2	80.8	218922	5	AL029292	AL029292 Zebrafish
5	19.8	79.2	89317	2	AC025121	AC025121 Homo sapi
6	19.8	79.2	150154	9	AL391477	AL391477 Human DNA
7	19.8	79.2	157280	2	AC022378	AC022378 Homo sapi
8	19.4	77.6	1243	1	AY212597	AY212597 Unculture
9	19.2	76.8	2423	4	AB028866	AB028866 Bos tauru
10	19.2	76.8	40304	6	AX695905	AX695905 Sequence
11	19.2	76.8	86574	6	C0861540	C0861540 Sequence
12	19.2	76.8	86574	9	HS93387	HS93387 Human DNA
13	19.2	76.8	89566	9	AL390204	AL390204 Human DNA
14	19.2	76.8	110000	2	AL672265	AL672265 2
15	19.2	76.8	123325	8	AP006116	AP006116 Lotus cor
16	19.2	76.8	151851	2	AC009157	AC009157 Homo sapi
17	19.2	76.8	163217	9	AF336797	AF336797 Homo sapi
18	19.2	76.8	173627	9	AC099511	AC099511 Homo sapi
19	19.2	76.8	179168	2	AC009071	AC009071 Homo sapi

C 20	19.2	76.8	195189	2	AC034149	AC034149 Homo sapi
C 21	19.2	76.8	279177	2	AC146652	AC146652 Pan trogl
C 22	18.8	75.2	106346	9	AC004045	AC004045 Homo sapi
C 23	18.8	75.2	153624	9	HS1018K9	AL031726 Human DNA
C 24	18.8	75.2	164736	2	AL390855	AL390855 Homo sapi
C 25	18.8	75.2	189876	2	AC084810	AC084810 Homo sapi
C 26	18.8	75.2	226791	2	AC094199	AC094199 Rattus no
C 27	18.8	75.2	227208	2	AC150218	AC150218 Callithri
C 28	18.6	74.4	10670	1	U32781	U32781 Haemophilus
C 29	18.6	74.4	63798	2	AC124310	AC124310 Homo sapi
C 30	18.6	74.4	110000	6	BD426631	BD426631 10
C 31	18.6	74.4	110000	6	AR274513	AR274513 10
C 32	18.6	74.4	110000	6	AR541453	AR541453 10
C 33	18.6	74.4	148326	2	AC103619	AC103619 Mus muscu
C 34	18.6	74.4	148344	10	AC090432	AC090432 Mus muscu
C 35	18.6	74.4	156997	9	AC011465	AC011465 Homo sapi
C 36	18.6	74.4	164291	9	AC021351	AC021351 Homo sapi
C 37	18.6	74.4	165408	2	AC122425	AC122425 Mus muscu
C 38	18.6	74.4	167167	2	AC012035	AC012035 Homo sapi
C 39	18.6	74.4	167550	2	EX296544	EX296544 Danio rer
C 40	18.6	74.4	170807	9	AC124307	AC124307 Homo sapi
C 41	18.6	74.4	171224	2	AC091600	AC091600 Homo sapi
C 42	18.6	74.4	177302	10	AC127415	AC127415 Mus muscu
C 43	18.6	74.4	183089	10	AL663115	AL663115 Mouse DNA
C 44	18.6	74.4	189650	10	AC136091	AC136091 Rattus no
C 45	18.6	74.4	191925	9	AC147386	AC147386 Pan trogl

ALIGNMENTS

RESULT 1	AC124978	182405 bp	DNA	linear	ROD 13-APR-2004
LOCUS	Mus musculus chromosome 5, clone RP24-107D19, complete sequence.				
DEFINITION	AC124978				
ACCESSION	AC124978.19	GI:46359995			
VERSION	HTG.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 182405)				
AUTHORS	Birren, B., Nusbaum, C. and Lander, E.				
TITLE	Mus musculus chromosome 5, clone RP24-107D19				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 182405)				
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliiev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakocque, K., Lamazares, R., Landers, T., Lechoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, P., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA				
REFERENCE	3 (bases 1 to 182405)				

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collamore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreika, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrum, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, C., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 182405)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,
Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J.,
Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B.,
DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,
Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, C., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
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O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R.,
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Stojanovic, N., Stubbs, M., Talamas, D., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

SMITH, A.F.A. & GREEN, F. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center -----
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIGR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submission@consbroad.mit.edu
----- Project Information -----
Center project name: L24353
Center clone name: 107 D 19

Some of the sequence contained within base pairs 96927 to the end of the clone was stolen from accession AC127332.

FEATURES

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Query Match 81.6%; Score 20.4; DB 9; Length 27745;
 Best Local Similarity 68.2%; Pred. No. 43;
 Matches 15; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ACUCAGGAUUCAGAUAGCC 24
 ||:||||:||||:|
 Db 6933 ACTTCAGGATTCAGATATGTC 6912

RESULT 4
 AL929292 218922 bp DNA linear VRT 23-SEP-2003
 LOCUS Zebrafish DNA sequence from clone DKEY-11L24 in linkage group 14,
 DEFINITION complete sequence.
 ACCESSION AL929292.7 GI:34996460
 VERSION AL929292
 KEYWORDS HTG.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 218922)
 Direct Submission
 Submitted (23-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Sep 23, 2003 this sequence version replaced gi:28445772.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Web site: http://www.sanger.ac.uk
 Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep DKEY-11L24 is from a Zebrafish BAC library

VECTOR: pIndigoBAC-5
 Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml.

FEATURES

Location/Qualifiers
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ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 218922;
 Best Local Similarity 68.0%; Pred. No. 60;
 Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CAACUUCAGGAUUCAGAUAGCC 25
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 Db 185663 CAACTTCAGCATTCAGAAATGCAC 185687

RESULT 5
 AC025121/c
 LOCUS Homo sapiens chromosome 1 clone RP11-21M14 map 1, LOW-PASS SEQUENCE
 DEFINITION SAMPLING.
 ACCESSION AC025121.1 GI:7158932
 VERSION AC025121
 KEYWORDS HTG; HTGS PHASE0.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 89317)
 Homo sapiens chromosome 1, clone RP11-21M14
 Unpublished
 2 (bases 1 to 89317)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castile,A., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Donino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieue,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrin,J., Meneus,L., Mihova,T., Miranda,C., Menga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thoman,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (05-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIER
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L7580
 Center clone name: 21_M_14

***** NOTE: This record contains 93 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that

* the record is updated, the accession number will
* be preserved.

1 854: contig of 854 bp in length
* 855 954: gap of 100 bp
* 955 1814: contig of 860 bp in length
* 1815 1914: gap of 100 bp
* 1915 2754: contig of 840 bp in length
* 2755 2854: gap of 100 bp
* 2855 3711: contig of 857 bp in length
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* 3812 4677: contig of 866 bp in length
* 4678 4777: gap of 100 bp
* 4778 5649: contig of 872 bp in length
* 5650 5749: gap of 100 bp
* 5750 6564: contig of 815 bp in length
* 6565 6664: gap of 100 bp
* 6665 7532: contig of 868 bp in length
* 7533 7632: gap of 100 bp
* 7633 8487: contig of 855 bp in length
* 8488 8587: gap of 100 bp
* 8588 9448: contig of 861 bp in length
* 9449 9548: gap of 100 bp
* 9549 10414: contig of 866 bp in length
* 10415 10514: gap of 100 bp
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* 11389 11488: gap of 100 bp
* 11489 12327: contig of 839 bp in length
* 12328 12427: gap of 100 bp
* 12428 13288: contig of 861 bp in length
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* 14242 14341: gap of 100 bp
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* 15209 15308: gap of 100 bp
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* 16153 16252: gap of 100 bp
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* 18066 18165: gap of 100 bp
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* 37378 37477: gap of 100 bp
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* 39411 40279: contig of 869 bp in length
* 40280 40379: gap of 100 bp
* 40380 41245: contig of 886 bp in length
* 41246 41345: gap of 100 bp
* 41346 42196: contig of 851 bp in length
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* 49961 50821: contig of 861 bp in length
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* 52837 53700: contig of 864 bp in length
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* 54666 54765: gap of 100 bp
* 54766 55687: contig of 922 bp in length
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* 55788 56623: contig of 836 bp in length
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* 57691 58550: contig of 860 bp in length
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* 58651 59526: contig of 876 bp in length
* 59527 59626: gap of 100 bp
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* 60507 60606: gap of 100 bp
* 60607 61469: contig of 863 bp in length
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* 61570 62438: contig of 869 bp in length
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* 62539 63364: contig of 826 bp in length
* 63365 63464: gap of 100 bp
* 63465 64326: contig of 862 bp in length
* 64327 64426: gap of 100 bp
* 64427 65281: contig of 855 bp in length
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* 65382 66196: contig of 815 bp in length
* 66197 66296: gap of 100 bp

Query Match 79.2%; Score 19.8; DB 2; Length 89317;
Best Local Similarity 69.6%; Pred. No. 92;
Matches 16; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUUCACAGUAUUGCC 24

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Db 13870 AACTTCAGGATTCAGAAATTC 13848
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RESULT 6
AL391477/c
LOCUS 150154 bp DNA linear PRI 17-JUL-2002
DEFINITION Human DNA sequence from clone RP11-21M14 on chromosome 1, complete
sequence.
ACCESSION AL391477
VERSION AL391477.20 GI:21911468
KEYWORDS Homo sapiens (human)
SOURCE HTG.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 150154)
JOURNAL Direct Submission
COMMENT Submitted (16-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 19, 2002 this sequence version replaced gi:21537432.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl
RP11-21M14 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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FEATURES
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Best Local Similarity 69.6%; Pred. No. 94;
Matches 16; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 AACUUCAGGUAUCCAGUAUCC 24
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Db 120469 AACTTCAGGATTCAGAAATTC 120447
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QY 2 AACUUCAGGAUUCAGAUUGCC 24
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Db 22869 AACTTCAGGATCCAGAAATCC 22891

RESULT 8
AY212597/c 1243 bp DNA linear BCT 16-JAN-2004
LOCUS Uncultured bacterium clone 146ds20 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AY212597
VERSION AY212597.1 GI:37786996
KEYWORDS uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 1243)
AUTHORS Simpson,J.M., Santo Domingo,J.W. and Reasoner,D.J.
TITLE Assessment of equine fecal contamination: the search for
alternative bacterial source-tracking targets
JOURNAL FEMS Microbiol. Ecol. 47 (1), 65-75 (2004)
REFERENCE 2 (bases 1 to 1243)
AUTHORS Simpson,J.M., Santo Domingo,J.W. and Reasoner,D.J.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Office of Research and Development - Water
Supply Water Resources Division, U.S. Environmental Protection
Agency, 26 W. Martin Luther King Dr., Cincinnati, OH 45268, USA
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Query Match 77.6%; Score 19.4; DB 1; Length 1243;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 15; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 CUUCAGGAUUCAGAUUGCC 24
||||:||||:||||:||||:|
Db 1001 CTTGAGGATCCAGATGCC 981

RESULT 9
ABO28866/c 2423 bp mRNA linear MAM 17-JUN-1999
LOCUS Bos taurus mRNA for prollyl oligopeptidase, complete cds.
DEFINITION ABO28866
ACCESSION ABO28866
VERSION ABO28866.1 GI:5103284
KEYWORDS prollyl oligopeptidase.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (sites)
AUTHORS Yoshimoto,T., Miyazaki,K., Haraguchi,N., Kitazono,A., Kabashima,T.
and Ito,K.
TITLE Cloning and expression of the cDNA encoding prollyl oligopeptidase
JOURNAL Biol. Pharm. Bull. 20 (10), 1047-1050 (1997)
MEDLINE 98014979
PUBMED 9353562
REFERENCE 2 (bases 1 to 2423)
AUTHORS Yoshimoto,T., Miyazaki,K., Haraguchi,N., Kitazono,A., Kabashima,T.
and Ito,K.
TITLE Direct Submission

QY 1 CAACUUCAGGAUUCAGAUUGCC 24
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Db 956 CCATTTCAGGATCCAGTGATGCC 933

RESULT 10
AX695905/c 40304 bp DNA linear PAT 31-MAR-2003
LOCUS AX695905
DEFINITION Sequence 1532 from Patent WO03008583.
ACCESSION AX695905
VERSION AX695905.1 GI:29419070
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Morris,D.W. and Engelhard,E.K.
TITLE Novel compositions and methods for cancer
JOURNAL Patent: WO 03008583-A 1532 30-JAN-2003;
Sagres Discovery (US)
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ORIGIN
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Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCAGAUUGCC 25
||||:||||:||||:||||:|
Db 37678 AACTTGAGGATCCAGATATTC 37655

JOURNAL Submitted (10-JUN-1999) Teutomu Kabashima, School of Pharmaceutical
Sciences Nagasaki University, Department of Biotechnology; 1-14
Bunkyo-machi, Nagasaki, Nagasaki 852-8521, Japan
(E-mail:t-kabashima@cc.nagasaki-u.ac.jp,
Tel:81-95-847-1111(ex.2552), Fax:81-95-843-2444)
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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/tissue_lib="brain"
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/protein_id="BAA78907.1"
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QSEDIKCAEFDPDEPKMGGAEISDDGRYLLSIREGCDPVNRLWYCDLHQBPNGITGI
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KDVLEWACVRSNPLVLCYLDHDKVNTLQLDHDMATGALLKTFPLEVGSVVGSGOKDIT
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RPDIFGCVIAGVMDMLKFHYTHIAWTTDYGCSNKHQFELIKTSPLHNKVLPE
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ORIGIN
Query Match 76.8%; Score 19.2; DB 4; Length 2423;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCAGAUUGCC 24
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Db 956 CCATTTCAGGATCCAGTGATGCC 933

RESULT 10
AX695905/c 40304 bp DNA linear PAT 31-MAR-2003
LOCUS AX695905
DEFINITION Sequence 1532 from Patent WO03008583.
ACCESSION AX695905
VERSION AX695905.1 GI:29419070
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Morris,D.W. and Engelhard,E.K.
TITLE Novel compositions and methods for cancer
JOURNAL Patent: WO 03008583-A 1532 30-JAN-2003;
Sagres Discovery (US)
FEATURES
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ORIGIN
Query Match 76.8%; Score 19.2; DB 6; Length 40304;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCAGAUUGCC 25
||||:||||:||||:||||:|
Db 37678 AACTTGAGGATCCAGATATTC 37655

```

RESULT 11
 CQ861540/c
 LOCUS
 DEFINITION
 ACCESSION
 CQ861540
 VERSION
 CQ861540.1
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1
 Burczynski.M., Twine.N., Dörner.A.J. and Trepicchio.W.L.
 METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO / I
 Patent: WO 2004072265-A 173 26-AUG-2004;
 Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
 Dörner, Andrew J. (US); Trepicchio, William L. (US)
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 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AACUACGAGAUCCAGAUAGCCC 25
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 Db 36754 AACTGAGGATGCCAGATATCCC 36731
 RESULT 12
 HS833B7/c
 LOCUS
 DEFINITION
 Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2
 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD),
 the 5' part of the CSF2RB gene for granulocyte-macrophage
 low-affinity colony stimulating factor 2 receptor beta, ESRs, STS
 and GSSs, complete sequence.
 AL008637
 AL008637.1 GI:3136000
 HTG; colony stimulating factor; CSF2RB; cytosolic neutrophil
 factor; NCF4.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1
 Burton.J.
 TITLE
 Direct Submission
 Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk
 Clone requests: clonerequest@sanger.ac.uk
 On May 18, 1998 this sequence version replaced gi:2578146.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep CTA-833B7 is
 from the human BAC library described in U-J. Kim et al. (1996)
 Genomics 34, 213-218.
 VECTOR: pBelOBAcl11
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC

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repeat_region /note="L1ME1 repeat: matches 5523. .5604 of consensus"
repeat_region complement(5371. .5676)
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repeat_region 5677. .6268
repeat_region /note="L1ME1 repeat: matches 5604. .6332 of consensus"
repeat_region 6302. .6481
repeat_region /note="L2 repeat: matches 2636. .2819 of consensus"
repeat_region complement(6483. .6755)
repeat_region /note="MERL15 repeat: matches 393. .688 of consensus"
repeat_region 6934. .6962
repeat_region /note="2.1 copies 14 mer TGCATGTATGTGCA 49% conserved"
repeat_region 6944. .6953
repeat_region /note="2.5 copies 4 mer TGCA 20% conserved"
repeat_region 6984. .7002
repeat_region /note="1.9 copies 10 mer TGCAGGTGTG 29% conserved"
repeat_region 6999. .7085
repeat_region /note="6.2 copies 14 mer GTGTATATGTACAT 66% conserved"
repeat_region 7000. .7014
repeat_region /note="2.5 copies 6 mer TGTACA 30% conserved"
repeat_region 7006. .7022
repeat_region /note="2.1 copies 8 mer TGTACATG 25% conserved"
repeat_region 7047. .7193
repeat_region /note="6.1 copies 24 mer GTGTGATGTGTATATGTGCTGC 113% conserved"
repeat_region 7048. .7080
repeat_region /note="5.5 copies 6 mer TGTGTA 30% conserved"
repeat_region 7053. .7085
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repeat_region 7118. .7127
repeat_region /note="2.5 copies 4 mer TGCA 20% conserved"
repeat_region 7125. .7136
repeat_region /note="2.0 copies 6 mer ATGTGT 24% conserved"
repeat_region 7148. .7164
repeat_region /note="2.8 copies 6 mer TGTGTA 25% conserved"
repeat_region 7203. .7332
repeat_region /note="L2 repeat: matches 3165. .3313 of consensus"
repeat_region 7333. .7342
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repeat_region 7347. .7532
repeat_region /note="MIR repeat: matches 2. .191 of consensus"
repeat_region complement(7537. .7640)
repeat_region /note="MIR repeat: matches 158. .262 of consensus"
repeat_region complement(8152. .8228)
repeat_region /note="MIR repeat: matches 184. .260 of consensus"
repeat_region 8253. .8341
repeat_region /note="L2 repeat: matches 3214. .3311 of consensus"
repeat_region 8504. .8516
repeat_region /note="2.6 copies 5 mer AGAGA 26% conserved"
repeat_region 8848. .8859
repeat_region /note="2.0 copies 6 mer AGTTCC 24% conserved"
repeat_region 9588. .9602
repeat_region /note="5.0 copies 3 mer GCA 21% conserved"
repeat_region 9920. .9935
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repeat_region 10428. .10439
repeat_region /note="3.0 copies 4 mer TGCT 24% conserved"
repeat_region 10570. .10580
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gene 11913. .29288
gene /gene="NCF4"
mRNA join(11913. .12573,15415. .15499,16289. .16442,18762. .18832,
21785. .21912,23022. .23079,23697. .23795,27023. .27153,
27399. .27464,28998. .29288)
gene /gene="NCF4"
/product="bkr83387.1 (neutrophil cytosolic factor 4
(40kD))"
/note="match: cDNAs: Em:AB002665 Em:X77094 Em:U59488
match: ESTs: Em:AA177839 Em:AI007048 Em:AA465462
Em:AA465389 Em:AA485518 Em:AI381940 Em:AA744805
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Em:AA975113 Em:AA969460 Em:AA948430 Em:AI435296
Em:AI299103 Em:AA648472 Em:AA702857 Em:AI089359 Em:D20144
Em:AA909156 Em:AA68071 Em:W95229 Em:AI439568"
/evidence=not_experimental
complement(11982. .12109)
/note="L2 repeat: matches 2918. .3064 of consensus"
repeat_region 12358. .12367
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repeat_region 12443. .12453
repeat_region /note="2.2 copies 5 mer GAGAC 22% conserved"
CDS join(12542. .12573,15415. .15499,16289. .16442,18762. .18832,
21785. .21912,23022. .23079,23697. .23795,27023. .27153,
27399. .27464,28998. .29193)
/gene="NCF4"
/note="match: proteins: Tr:O60808 Tr:P97369"
/codon_start=1
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Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUCCAGAUUGCCC 25
Db 36754 AACTTGAGGATCCAGATATCCC 36731
||||:||||:||||:||||:||||:
AL390204 89566 bp DNA linear PRI 15-NOV-2001
Human DNA sequence from clone Rp11-196D4 on chromosome 1, complete
sequence.
ACCESSION AL390204
VERSION AL390204.11 GI:16972946
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Smith.M.
Direct Submission
Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humqu@sanger.ac.uk
On Nov 16, 2001 this sequence version replaced gi:16151421.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Swi,
SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WormPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
Rp11-196D4 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
Rp11-196D4 it may be shorter because we sequence overlapping
```

sections only once, except for a short overlap.
The true left end of clone RP11-196D4 is at 1 in this sequence. The
true left end of clone RP11-307C12 is at 87567 in this sequence.

FEATURES

source
1. .89566
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-196D4"
/clone_lib="RPC1-11.1"

ORIGIN

Query Match 76.8%; Score 19.2; DB 9; Length 89566;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUUGCCC 25
|| : ||||: ||||: ||||: ||||
DB 74674 AATTCAGGATTCAGCTATGCC 74697

RESULT 14

AL672265.2/c

WPCOMMENT

Sequence split into 6 fragments LOCUS AL672265 Accession AL672265

Fragment Name	Begin	End
AL672265_0	1	110000
AL672265_1	100001	210000
AL672265_2	200001	310000
AL672265_3	300001	410000
AL672265_4	400001	510000
AL672265_5	500001	534015

Continuation (3 of 6) of AL672265 from base 200001 (AL672265 Homo sapiens chromosome 1)

Query Match 76.8%; Score 19.2; DB 2; Length 110000;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUUGCCC 25
|| : ||||: ||||: ||||: ||||
DB 21515 AATTCAGGATTCAGCTATGCC 21492

RESULT 15

AP006116/c

LOCUS

AP006116 123325 bp DNA linear PLN 22-JUL-2003
Lotus corniculatus var. japonicus genomic DNA, chromosome 1,
clone:LjT40C04, TW0199, complete sequence.

ACCESSION

AP006116

VERSION

AP006116.1 GI:29122755

KEYWORDS

HTG.

SOURCE

Lotus corniculatus var. japonicus (Lotus japonicus)

ORGANISM

Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

REFERENCE
1
Kaneko,T., Asamizu,E., Kato,T., Sato,S., Nakamura,Y. and Tabata,S.
Structural analysis of a Lotus japonicus genome. III. Sequence
features and mapping of sixty-two TAC clones which cover the 6.7 Mb
regions of the genome
DNA Res. 10 (1), 27-33 (2003)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

Submitted (12-DEC-2002) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba 232-0818, Japan (E-mail:bsato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),

Fax:81-438-52-3934)

FEATURES

source

1. .123325
Location/Qualifiers
/organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/variety="japonicus"
/db_xref="taxon:34305"
/chromosome="1"
/clone="LjT40C04"
/clone_lib="LjT library"
/note="TAC clone:TW0199-synonym: Lotus japonicus"

ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 123325;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACTUCAGGAUCCAGAUUGCCC 24
||||:||||:||||:||||: ||||
DB 25756 CAACTTCAGGATTCAGATAATCC 25733

Search completed: July 30, 2005, 12:54:28

Job time : 736.757 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:32:26 ; Search time 308.446 Seconds
(without alignments)
479.804 Million cell updates/sec

Title: US-09-544-776-4
Perfect score: 25
Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

1:	Geneseqn1980s:*
2:	Geneseqn1990s:*
3:	Geneseqn2000s:*
4:	Geneseqn2001as:*
5:	Geneseqn2001bs:*
6:	Geneseqn2002as:*
7:	Geneseqn2002bs:*
8:	Geneseqn2003as:*
9:	Geneseqn2003bs:*
10:	Geneseqn2003cs:*
11:	Geneseqn2003ds:*
12:	Geneseqn2004as:*
13:	Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3 AAC64408	AAC64408 Human Nog
C 2	19.2	76.8	270	6 ABL70775	ABL70775 Corn tass
C 3	19.2	76.8	40304	9 ADA03014	ADA03014 Human NCF
C 4	19.2	76.8	40304	10 ADB72752	ADB72752 Human NCF
C 5	19.2	76.8	40304	10 ADC85494	ADC85494 Human Ncf
C 6	19.2	76.8	40304	12 ADM74609	ADM74609 Human car
C 7	19.2	76.8	86574	6 ABR33560	ABR33560 Human cDN
C 8	19.2	76.8	86574	13 ADR52822	ADR52822 Drug ther
9	18.6	74.4	391	8 ABX43504	ABX43504 Bovine ES
10	18.6	74.4	402	8 ABX45854	ABX45854 Bovine ES
11	18.6	74.4	422	8 ABX40707	ABX40707 Bovine ES
12	18.6	74.4	609	4 AAK86539	AAK86539 Human imm
C 13	18.6	74.4	110000	2 AAR42063_10	Continuation (11 o
C 14	18.4	73.6	8473	2 AAL025487	AAL025487 Human myo
C 15	18.2	72.8	2969	4 ABL02346	ABL02346 Drosophill
C 16	18.2	72.8	4530	4 ABL26458	ABL26458 Drosophill
C 17	17.6	70.4	460	9 ACH21863	ACH21863 Human adu
C 18	17.6	70.4	569	4 AAK94059	AAK94059 Human cDN
C 19	17.6	70.4	569	12 ADL30486	ADL30486 3' end of
20	17.6	70.4	576	4 AAK63128	AAK63128 Human imm

21	17.6	70.4	1362	4 ABL21915	ABL21915 Drosophill
22	17.6	70.4	1379	3 AAC59134	AAC59134 Human sec
23	17.6	70.4	1441	12 ADQ25167	ADQ25167 Human sof
C 24	17.6	70.4	1994	4 AAI114791	AAI114791 Probe #47
C 25	17.6	70.4	1994	4 ABA56518	ABA56518 Human foe
C 26	17.6	70.4	1994	4 AAI36149	AAI36149 Probe #48
C 27	17.6	70.4	1994	4 ABA45986	ABA45986 Human bre
C 28	17.6	70.4	1994	4 ABA26148	ABA26148 Probe #46
C 29	17.6	70.4	1994	4 AAK30186	AAK30186 Human bon
C 30	17.6	70.4	1994	4 AAK04674	AAK04674 Human bra
C 31	17.6	70.4	1994	4 ABS29836	ABS29836 Human liv
C 32	17.6	70.4	1994	5 AAI04584	AAI04584 Probe #45
C 33	17.6	70.4	1994	6 ABS04773	ABS04773 Human gen
C 34	17.6	70.4	2130	2 AAK98543	AAK98543 Prolyl en
C 35	17.6	70.4	2562	8 ACC49473	ACC49473 Human pro
C 36	17.6	70.4	2562	10 ADE38352	ADE38352 Human pro
C 37	17.6	70.4	2562	13 ADR40162	ADR40162 Human pro
38	17.6	70.4	2712	10 ADB62183	ADB62183 Human cDN
C 39	17.6	70.4	2756	10 ADG89414	ADG89414 Cancer de
40	17.6	70.4	3362	4 ABL21914	ABL21914 Drosophill
41	17.6	70.4	3923	4 ABL21916	ABL21916 Drosophill
42	17.6	70.4	4744	4 AAS03072	AAS03072 Human dia
43	17.6	70.4	19696	4 AAL06639	AAL06639 Human rep
44	17.6	70.4	19696	5 AAS40722	AAS40722 DNA encod
45	17.6	70.4	19696	11 ADJ09928	ADJ09928 Human pro

ALIGNMENTS

RESULT 1
AAC64408
ID AAC64408 standard; RNA; 25 BP.
XX AC AAC64408;
XX DT 08-FEB-2001 (first entry)
XX DE Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:4.
XX KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
XX KW stress-phosphorylated endoplasmic reticulum protein; cytostatic;
XX KW gene therapy; cell growth; cellular stress response; neuron growth;
XX KW regulator of oxidative stress; inhibitor of neurite outgrowth;
XX KW axon regeneration; diagnosis; cancer; identification; antisense;
XX KW phosphorothioate; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..25
FT /*tag= a
FT /note= "phosphorothioate linkages"

WO2000060083-A1.
12-OCT-2000.
07-APR-2000; 2000WO-US009383.
08-APR-1999; 99US-0128372P.
21-JUN-1999; 99US-0140331P.
(CHIR) CHIRON CORP.
Wei D, Halenbeck R, Williams LT;
WPI; 2000-665007/64.
Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic reticulum protein, designated Nogo B. Nogo B has cytoskeletal activity and is a modulator of the storage and exchange of calcium, cell growth and cellular stress response. It can regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polynucleotides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B polypeptides. The present sequence represents a human Nogo B phosphothioate antisense oligonucleotide from the present invention

XX Sequence 25 BP; 7 A; 8 C; 4 G; 0 T; 6 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 3; Length 25;

XX Best Local Similarity 100.0%; Pred. No. 0.046;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGCCC 25

DB 1 CAACUUCAGGAUCCAGAUAGCCC 25

RESULT 2

ABL70775/c

ID ABL70775 standard; cDNA; 270 BP.

XX AC ABL70775;

XX 14-MAY-2002 (first entry)

XX Corn tassal-derived polynucleotide (cdps) SEQ ID NO:149.

XX Corn; corn tassal-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassal; gene; ss.

XX Zea mays.

XX US2001051335-A1.

XX 13-DEC-2001.

XX 16-APR-1999; 99US-00294093.

XX 21-APR-1998; 98US-0082567P.

XX (LALG/) LALGUDI R V.

XX (ITOL/) ITO L Y.

XX (SHER/) SHERMAN B K.

XX Lalgudi RV, Ito LY, Sherman BK;

XX WPI; 2002-163647/21.

XX Novel purified corn tassal-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs.

XX Claim 1; SEQ ID NO 149; 201pp; English.

XX The present sequence describes a purified corn tassal-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76833. The cdps sequences encode corn tassal-derived polypeptides (CDPs). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable

CC characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassal-specific profile of gene transcription, a transcript image, to clone regulatory elements for use in transformation vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassal nucleic acid sequences from DNA libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid sequences

XX Sequence 270 BP; 61 A; 46 C; 65 G; 98 T; 0 U; 0 Other;

XX Query Match 76.8%; Score 19.2; DB 6; Length 270;

XX Best Local Similarity 62.5%; Pred. No. 40;

XX Matches 15; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUAGCCC 25

DB 46 ATCTTCAGCATTCAGATATGACC 23

RESULT 3

ADA03014/c

ID ADA03014 standard; DNA; 40304 BP.

XX AC ADA03014;

XX 06-NOV-2003 (first entry)

XX Human NCF4 carcinoma associated gene, SEQ ID NO:1532.

XX Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening; gene; ds.

XX Homo sapiens.

XX WO2003057146-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041414.

XX 26-DEC-2001; 2001US-00035832.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-587068/55.

XX New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.

XX Claim 1; SEQ ID NO 1532; 245pp; English.

XX The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose

CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukaemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed human CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;

Query Match 76.8%; Score 19.2; DB 9; Length 40304;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCC 25

Db 37678 AACTTGAGGATGCCAGATATTC 37655

RESULT 4

ADB72752/c
ID ADB72752 standard; DNA; 40304 BP.

XX AC

ADB72752;

DT 04-DEC-2003 (first entry)

XX DE Human NCF4 gene.

XX human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.

XX OS Homo sapiens.

XX PN WO2003008583-A2.

XX PD 30-JAN-2003.

PF 26-DEC-2001; 2001WO-US051291.

PR 02-MAR-2001; 2001US-00798586.

PR 23-OCT-2001; 2001US-00004113.

PR 08-NOV-2001; 2001US-00052482.

PR 30-NOV-2001; 2001US-00997722.

PR 20-DEC-2001; 2001US-00034650.

XX (SAGR-) SAGRES DISCOVERY.

XX PI Morris DW, Engelhard EK;

XX WPI; 2003-239337/23.

XX Claim 1; SEQ ID NO 580; 2304pp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytostatic
CC activity, and may have a use in gene therapy, or in a vaccine. The
CC recombinant nucleic acids and polypeptides are useful for treating
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC sarcomas. The present sequence represents a human gene of the invention.

XX SQ Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;

Query Match 76.8%; Score 19.2; DB 10; Length 40304;

Best Local Similarity 66.7%; Pred. No. 82;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCC 25
Db 37678 AACTTGAGGATGCCAGATATTC 37655

RESULT 5

ADC85494/c
ID ADC85494 standard; DNA; 40304 BP.

XX AC

ADC85494;

DT 01-JAN-2004 (first entry)

XX Human Ncf4 genomic sequence.

XX Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;
KW secreted; transmembrane; intracellular; ds.

XX OS Homo sapiens.

XX PN WO2003045230-A2.

XX PD 05-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038582.

XX PR 30-NOV-2001; 2001US-00997722.

XX PA (SAGR-) SAGRES DISCOVERY.

XX PI Morris DW, Engelhard EK;

XX WPI; 2003-513603/48.

XX New recombinant nucleic acid comprising a nucleotide sequence of any of
PT the carcinoma-associated (CA) genes, useful for screening for drug
PT candidates for diagnosing or treating carcinomas.

XX Claim 1; SEQ ID NO 280; 983pp; English.

XX The invention relates to a recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the fully defined carcinoma-
CC associated (CA) genes from the 50 tables given in the specification. The
CC CA proteins are secreted, transmembrane or intracellular proteins. The
CC recombinant nucleic acids are useful for screening for drug candidates
CC for diagnosing or treating carcinomas. Sequences given in ADC85515-
CC ADC85514 represent CA genes of the invention.

XX SQ Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;

Query Match 76.8%; Score 19.2; DB 10; Length 40304;

Best Local Similarity 66.7%; Pred. No. 82;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCC 25

Db 37678 AACTTGAGGATGCCAGATATTC 37655

RESULT 6

ADM74609/c
ID ADM74609 standard; DNA; 40304 BP.

XX AC

ADM74609;

DT 01-JUL-2004 (first entry)

XX Human carcinoma associated (CA) nucleic acid #139.

XX Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
KW carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
KW cytostatic.

XX	Homo sapiens.	ABK83560;	XX
OS	US2004072154-A1.	14-AUG-2002 (first entry)	AC
PN	15-APR-2004.	Human cDNA differentially expressed in granulocytic cells #131.	DT
XX	30-NOV-2001; 2001US-00997722.		XX
XX	22-DEC-2000; 2000US-00747377.	Human; ss; granulocytic cell; DNA chip; bacterial infection;	KW
PR	02-MAR-2001; 2001US-00798586.	viral infection; parasitic infection; protozoal infection;	KW
XX	(MORRIS/) MORRIS D W.	fungal infection; sterile inflammatory disease; psoriasis;	KW
PA	(ENGELHARD E K.	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;	KW
XX	Morris DW, Engelhard EK;	cardiac reperfusion injury; renal reperfusion injury; ARDS;	KW
XX	WPI; 2004-328562/30.	adult respiratory distress syndrome; inflammatory bowel disease;	KW
DR	New carcinoma associated gene or protein, useful for preparing a	Crohn's disease; ulcerative colitis; periodontal disease;	KW
XX	composition for diagnosing or treating carcinoma e.g., leukemia or	granulocyte activation; chronic inflammation; allergy.	XX
PT	lymphoma.		OS
PT			XX
XX	Claim 1; SEQ ID NO 280; 29pp; English.		PN
XX	The invention relates to new recombinant nucleic acids. The invention		XX
CC	also relates to a host cell comprising a recombinant nucleic acid or		XX
CC	expression vector, an expression vector comprising a recombinant nucleic		PD
CC	acid, a recombinant protein, a method of screening for drug candidates, a		XX
CC	method of screening for a bioactive agent capable of binding to a		XX
CC	carcinoma associated protein (CAP) encoded by a nucleotide sequence, a		PF
CC	method of screening for a bioactive agent capable of modulating the		XX
CC	activity of a CAP, a method of evaluating the effect of a candidate		XX
CC	carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting		PR
CC	the activity of a CAP, a method of treating carcinomas, a method of		XX
CC	neutralising the effect of a CAP and a method of diagnosing carcinoma or		XX
CC	propensity to carcinoma. A method of evaluating the effect of a candidate		XX
CC	carcinoma drug comprises administering the drug to a patient, removing a		XX
CC	cell sample from the patient and determining alterations in the		XX
CC	expression or activation of a gene comprising the nucleotide sequence. A		XX
CC	method of diagnosing carcinoma comprises determining the expression of		XX
CC	one or more genes comprising the nucleic acid sequence in a first tissue		XX
CC	type of a first individual and comparing the expression of the gene from		XX
CC	a second normal tissue type from the first individual or a second		XX
CC	unaffected individual, where a difference in the expression indicates		XX
CC	that the first individual has carcinoma. A method of inhibiting the		XX
CC	activity of a CAP comprises binding an inhibitor to the CAP. Treating		XX
CC	carcinomas comprises administering to a patient an inhibitor of CAP.		XX
CC	Neutralising the effect of a CAP comprises contacting an agent specific		XX
CC	for the CAP. The polypeptide specifically binds to the protein encoded by		XX
CC	the nucleic acid. It comprises an antibody that specifically binds to the		XX
CC	protein encoded by the nucleic acid. The nucleic acids are useful for		XX
CC	preparing a composition for diagnosing or treating carcinoma e.g.,		XX
CC	leukaemia or lymphoma. This sequence represents a human carcinoma		XX
CC	associated (CA) nucleic acid of the invention. Note: The sequence data		XX
CC	for this patent did not form part of the invention. Note: The sequence data		XX
CC	obtained in electronic format directly from USPTO at		XX
CC	seqdata.uspto.gov/sequence.html.		XX
XX	Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;		XX
XX	Query Match 76.8%; Score 19.2; DB 12; Length 40304;		XX
XX	Best Local Similarity 66.7%; Pred. No. 82;		XX
XX	Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;		XX
QY	2 AACTUCAGGUAUCCAGAUAGCC 25		XX
Db	: : : :		XX
Db	37678 AACTTGAGATGCCAGATATCC 37655		XX
RESULT 7			XX
ABK83560/c			XX
ID	ABK83560 standard; cDNA; 86574 BP.		XX

ABK83560;

14-AUG-2002 (first entry)

Human cDNA differentially expressed in granulocytic cells #131.

Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2.

11-APR-2002.

03-OCT-2001; 2001WO-US030821.

03-OCT-2000; 2000US-0237189P.

(GENE-) GENE LOGIC INC.

Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J; WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 131; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GCA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 86574 BP; 22071 A; 20398 C; 21552 G; 22553 T; 0 U; 0 Other;
SQ Query Match 76.8%; Score 19.2; DB 6; Length 86574;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUCCAGAUAGCC 25
|||: |||: |||: |||: |||: |||:
Db 36754 AACTTGAGGATGCCAGATATCCC 36731

RESULT 8
ADRS2822/C
ID ADRS2822 standard; DNA; 86574 BP.
XX AC ADRS2822;
XX DT 18-NOV-2004 (first entry)
XX DE Drug therapy altered expressed gene #173.
XX KW drug activity monitoring; expression profile; gene expression;
KW peripheral blood sample; peripheral blood mononuclear cell; drug therapy;
KW CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;
KW mTOR; db.
XX OS Homo sapiens.
XX PN WO2004072265-A2.
XX PD 26-AUG-2004.
XX PF 11-FEB-2004; 2004WO-US004118.
XX PR 11-FEB-2003; 2003US-0446133P.
XX PR 03-APR-2003; 2003US-0459782P.
XX PR 23-JAN-2004; 2004US-0538246P.
XX (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A. J.
PA (TRBP/) TREPICCHIO W L.
XX Burczynski M, Twine N, Dorner AJ, Trepicchio WL;
WPI; 2004-642301/62.
XX Monitoring drug activities in vivo comprises comparing an expression
PT profile of a gene in a peripheral blood sample of a patient before and
PT after drug therapy.
XX Disclosure; SEQ ID NO 173; 136pp; English.
XX The invention relates to a method of monitoring drug activities in vivo
CC by comparing an expression profile of at least one gene in a peripheral
CC blood sample of a patient to a reference expression profile of the at
CC least one gene, where the at least one gene is differentially expressed
CC in peripheral blood mononuclear cells (PBMCs) of patients who have a non-
CC blood disease and are subjected to a drug therapy as compared to PBMCs
CC isolated from the patient before the drug therapy, and where the patient
CC has the non-blood disease and is being treated by the drug therapy. The
CC method, kit, and nucleic acid array are useful for monitoring drug
CC activities in vivo. The drug is especially CCI-779, an ester analogue of
CC the immunosuppressant rapamycin which is a potent inhibitor of the
CC mammalian target of rapamycin (mTOR). This sequence represents a gene
CC expressed in PBMC altered by the drug therapy. (Note: this sequence does
CC no form part of the printed specification but was obtained in electronic
CC format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).

XX Sequence 86574 BP; 22071 A; 20398 C; 21552 G; 22553 T; 0 U; 0 Other;
SQ

Query Match 76.8%; Score 19.2; DB 13; Length 86574;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUCCAGAUAGCC 25
|||: |||: |||: |||: |||: |||:
Db 36754 AACTTGAGGATGCCAGATATCCC 36731

RESULT 9
ABX43504
ID ABX43504 standard; CDNA; 391 BP.
XX AC ABX43504;
XX DT 21-FEB-2003 (first entry)
XX DE Bovine EST associated with lactation/muscle/fat deposition #8669.
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX OS Bos Taurus.
XX PN US2002137139-A1.
XX PD 26-SEP-2002.
XX PF 24-SEP-2001; 2001US-00960352.
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX (BYATT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
WPI; 2003-110599/10.
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX Claim 2; SEQ ID NO 8669; 245pp; English.
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid; where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in

PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 03-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Baraah SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 41351; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention
XX
SQ Sequence 609 BP; 152 A; 163 C; 172 G; 122 T; 0 U; 0 Other;
Query Match 74.4%; Score 18.6; DB 4; Length 609;
Best Local Similarity 72.0%; Pred. No. 88;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAACUUCAGGAUUCGAGUAUGCCC 25
||||| :||||| :||||| :|||||

Db 566 CAACCTCAGGACTCCAGTCATGCCCC 590
RESULT 13
AAT42063_10/c
Continuation (11 of 19) of AAT42063 from base 1000001 (Haemophilus influenzae complete g
WP Sequence split into 19 fragments LOCUS AAT42063 Accession Aat42063
WP Fragment Name Begin End
WP AAT42063_00 1 110000
WP AAT42063_01 100001 210000
WP AAT42063_02 200001 310000
WP AAT42063_03 300001 410000
WP AAT42063_04 400001 510000
WP AAT42063_05 500001 610000
WP AAT42063_06 600001 710000
WP AAT42063_07 700001 810000
WP AAT42063_08 800001 910000
WP AAT42063_09 900001 1010000
WP AAT42063_10 1000001 1110000
WP AAT42063_11 1100001 1210000
WP AAT42063_12 1200001 1310000
WP AAT42063_13 1300001 1410000
WP AAT42063_14 1400001 1510000
WP AAT42063_15 1500001 1610000
WP AAT42063_16 1600001 1710000
WP AAT42063_17 1700001 1810000
WP AAT42063_18 1800001 1830121
Query Match 74.4%; Score 18.6; DB 2; Length 110000;
Best Local Similarity 64.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAACUUCAGGAUUCGAGUAUGCCC 25
||||| :||||| :||||| :|||||
Db 71778 CAACCTCAGGATGCCCTTTATGCCC 71754
RESULT 14
AAX25487/c
ID AAX25487 standard; cDNA; 8473 BP.
XX
XX AC AAX25487;
XX
XX DT 02-AUG-1999 (first entry)
XX
XX DE Human myosin IXa cDNA.
XX
XX KW Myosin IXa; human; Bardet-Biedl syndrome; Usher syndrome; diagnosis;
XX therapy; hearing loss; deafness; retinitis pigmentosa; obesity;
XX hypogonadism; sterility; polydactyly; brachydactyly; syndactyly;
XX mental retardation; renal abnormality; kidney disease; hypertension;
XX diabetes; cardiovascular abnormality; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 243..7889
XX /tag= a
XX /product= "myosin IXa"
XX
XX PN W09919489-A1.
XX
XX PD 22-APR-1999.
XX
XX PF 14-OCT-1998; 98WO-US021971.
XX
XX PR 15-OCT-1997; 97US-0062858P.
XX PR 17-OCT-1997; 97US-0062241P.
XX PR 30-DEC-1997; 97US-0068953P.
XX
XX PA (CHIR) CHIRON CORP.
XX
XX Gorman SW, Welch J, Duhl D, Leng S, Adams A, Sheffield V;

PI Chiu CY;
XX WPI; 1999-277643/23.
DR P-PSDB; AAY05781.
XX
XX Myosin Ixa and cyclic nucleotide gated channel-15 polypeptides.
XX
XX Claim 11; Fig 2; 69pp; English.
XX
XX This is the nucleotide sequence of human myosin Ixa cDNA. An isolated
CC nucleotide sequence comprising the present sequence, or nucleotides 243-
CC 7085, 243-680, 683-2399, 959-977, 2404-2747, 3158-3740 or 6473-6899, is
CC claimed. The cDNA was isolated from a human BAC contig that spanned
CC chromosomal region 15p22-23; the Bardet-Biedl syndrome gene maps to this
CC locus. Myosin Ixa is thus useful in the study, diagnosis and therapy of
CC Bardet-Biedl syndrome and Usher syndrome. The invention discloses myosin
CC Ixa and cyclic nucleotide gated channel-15 (CNGC-15) polypeptides,
CC polynucleotides, and compositions containing these polypeptides,
CC polynucleotides, expression cassettes, transformed cells and antibodies.
CC Conditions that can be treated by CNGC-15 and/or myosin Ixa polypeptides,
CC agonists and antagonists additionally include hearing loss, retinitis
CC pigmentosa, obesity, hypogonadism, sterility, polydactyly, brachydactyly,
CC syndactyly, mental retardation, renal abnormalities, hypertension,
CC diabetes and cardiovascular abnormalities (all claimed). Methods for the
CC expression and detection of CNGC-15 and myosin Ixa nucleotides and
CC polypeptides are also provided
XX
SQ Sequence 8473 BP; 2703 A; 1736 C; 1891 G; 2143 T; 0 U; 0 Other;
Query Match 73.6%; Score 18.4; DB 2; Length 8473;
Best Local Similarity 65.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
OY 2 AACUUCAGGAUUCAGAUAU 21
DB 1595 AACTTCAGGATTACAGATAT 1576
|||:|||||:|||||:
|||:|||||:|||||:
RESULT 15
ABL02346/c
ID ABL02346 standard; cDNA; 2969 BP.
XX
XX ABL02346;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 1520.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US0009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR P-PSDB; ABB58243.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX

PS Claim 1; SEQ ID NO 1520; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2969 BP; 881 A; 625 C; 609 G; 854 T; 0 U; 0 Other;
Query Match 72.8%; Score 18.2; DB 4; Length 2969;
Best Local Similarity 65.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
OY 1 CAACUUCAGGAUUCAGAUUGC 23
DB 425 CAACUUCAGGAUUCAGAUUGC 403
|||:|||||:|||||:
|||:|||||:|||||:
Search completed: July 30, 2005, 12:18:08
Job time : 311.446 secs

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:50:11 ; Search time 2561.15 Seconds
(without alignments)
371.555 Million cell updates/sec

Title: US-09-544-776-4
Perfect score: 25
Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
C 1	25	100.0	388	1	AA100508
C 2	23.4	93.6	823	2	BF694585
C 3	23.4	93.6	925	2	BF789989
C 4	21.8	87.2	216	2	BF229985
C 5	21.8	87.2	370	9	CG573906
C 6	21.8	87.2	380	9	CG539807
C 7	21.8	87.2	601	2	BF570751
C 8	21.8	87.2	739	2	BF693401
C 9	21.8	87.2	863	4	BI668593
C 10	20.8	83.2	432	1	AI225530
C 11	20.8	83.2	515	8	AZ513867
C 12	20.8	83.2	673	1	AV726731
C 13	20.8	83.2	698	2	BF791086
C 14	20.2	80.8	473	1	AA193133
C 15	20.2	80.8	587	2	BF687772
C 16	20.2	80.8	587	4	BG427535
C 17	20.2	80.8	687	6	CA163435
C 18	20.2	80.8	757	2	BF791087
C 19	20.2	80.8	826	4	BG426667
C 20	20.2	80.8	845	2	BF672700
C 21	19.2	76.8	314	2	BE845938
C 22	19.2	76.8	317	7	CN253955
C 23	19.2	76.8	342	6	CD706840
C 24	19.2	76.8	414	2	AW066689

25	19.2	76.8	427	8	AQ633324
C 26	19.2	76.8	433	4	BG349404
C 27	19.2	76.8	499	7	CK944021
C 28	19.2	76.8	513	4	BG349720
C 29	19.2	76.8	518	6	CB455616
C 30	19.2	76.8	630	7	CK979258
C 31	19.2	76.8	647	4	BG866086
C 32	19.2	76.8	732	9	CE807695
C 33	19.2	76.8	895	2	BF681266
C 34	19.2	76.8	1180	2	BF790177
C 35	18.8	75.2	522	2	AW642399
C 36	18.8	75.2	551	8	AQ321144
C 37	18.8	75.2	666	6	BY734522
C 38	18.8	75.2	700	1	AL508468
C 39	18.6	74.4	303	7	CR465805
C 40	18.6	74.4	316	6	CB708790
C 41	18.6	74.4	318	1	AA892501
C 42	18.6	74.4	408	2	BE328934
C 43	18.6	74.4	420	2	BF416636
C 44	18.6	74.4	439	1	AI717137
C 45	18.6	74.4	510	4	BI541804

ALIGNMENTS

RESULT 1
AA100508/c
LOCUS AA100508 388 bp mRNA linear EST 01-DEC-1996
DEFINITION zn51c07.kl Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:561708 5' similar to TR:G307311 G307311 HISTONE H4. ;, mRNA sequence.
ACCESSION AA100508 GI:1646836
VERSION AA100508.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 388)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoso, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (infoimage.lbnl.gov) for further information.
Insert Length: 1132 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 319.
Location/Qualifiers
1. 388
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:4594998"
/db_xref="taxon:9606"
/clone="IMAGE:561708"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene muscle 937209"

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (infoimage.lbnl.gov) for further information.
Insert Length: 1132 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 319.
Location/Qualifiers
1. 388
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:4594998"
/db_xref="taxon:9606"
/clone="IMAGE:561708"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene muscle 937209"

/note="Organ: skeletal muscle; Vector: pBluescript SK-; Site 1: ECORI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Skeletal muscle from patient with malignant hyperthermia. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGACGACG 3' ~3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGT 3'.

ORIGIN

Query Match 100.0%; Score 25; DB 1; Length 388;
Best Local Similarity 76.0%; Pred. No. 1;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUAGCC 25
||||:||||:||||:||||:||||:
Db 375 CAACCTCAGGATTCAGATATGCC 351

RESULT 2

BF694585/c
LOCUS 602081409F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245770 5',
DEFINITION mRNA sequence.

ACCESSION BF694585
VERSION BF694585.1 GI:11979993
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI060 row: a column: 03

High quality sequence stop: 571.

FEATURES

source Location/Qualifiers

1..823

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4245770"

/lab_host="DH10B (TI phage-resistant)"

/clone_lib="NIH_MGC_81"

/note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGGCGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 93.6%; Score 23.4; DB 2; Length 823;
Best Local Similarity 72.0%; Pred. No. 6.6;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUAGCC 25
||||:||||:||||:||||:||||:
Db 401 CAACCTCAGGATTCAGATATGCC 377

RESULT 3

BF789989/c

LOCUS 602249960F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4328127 5',

DEFINITION mRNA sequence.

ACCESSION BF789989

VERSION BF789989.1 GI:12095025

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI187 row: h column: 16

High quality sequence stop: 527.

FEATURES

source Location/Qualifiers

1..925

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4328127"

/lab_host="DH10B (TI phage-resistant)"

/clone_lib="NIH_MGC_81"

/note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGGCGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 93.6%; Score 23.4; DB 2; Length 925;
Best Local Similarity 72.0%; Pred. No. 6.7;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUAGCC 25

||||:||||:||||:||||:||||:

Db 380 CAACCTCAGGATTCAGATATGCC 356

RESULT 4

BF229985

LOCUS MR2-CT0456-220900-004-e07 CT0456 Homo sapiens cDNA, mRNA sequence.

DEFINITION mRNA sequence.

ACCESSION BF229985

VERSION BF229985.1 GI:11167490

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,P., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=kt2=MR2-CT0456-220
900-004-e07kt3=2000-09-22kt4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 215.
Location/Qualifiers

FEATURES

source
1..216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0456"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 87.2%; Score 21.8; DB 2; Length 216;
Best Local Similarity 72.0%; Pred. No. 28;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCAGAUAGCC 25
|||::|||:||||:||||
Db 68 CAACTTCAGATCCAGATATGCC 92

RESULT 5

CG573906/c
LOCUS 370 bp mRNA linear GSS 02-OCT-2003
DEFINITION OST206109 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST206109,
mRNA sequence.

ACCESSION CG573906
VERSION CG573906.1 GI:37364243
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 370)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

TITLE

Query Match 87.2%; Score 21.8; DB 9; Length 380;
Best Local Similarity 68.0%; Pred. No. 32;
Matches 17; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCAGAUAGCC 25

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..370
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST206109"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 87.2%; Score 21.8; DB 9; Length 370;
Best Local Similarity 68.0%; Pred. No. 32;
Matches 17; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCAGAUAGCC 25
|||::|||:||||:||||
Db 136 CAACTTCAGATCCAGATATGCC 112

RESULT 6

CG539807/c
LOCUS 380 bp mRNA linear GSS 01-OCT-2003
DEFINITION OST131162 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST131162,
mRNA sequence.

ACCESSION CG539807
VERSION CG539807.1 GI:37326379
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 380)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

TITLE

JOURNAL
COMMENT

FEATURES

source
1..380
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST131162"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 87.2%; Score 21.8; DB 9; Length 380;
Best Local Similarity 68.0%; Pred. No. 32;
Matches 17; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCAGAUAGCC 25


```

FEATURES
  source
    High quality sequence stop: 689.
    Location/Qualifiers
      1..863
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:5313024"
        /tissue_type="hypothalamus"
        /lab_host="DH10B"
        /clone_lib="NIH MGC 96"
        /notes="Organ: Brain; Vector: pBluescriptR (modified
        pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
        (ctcag); Oligo-dT primed using primer
        5'-TTTTTTTTTTTTTNN-3', size-selected for average
        insert size 2.3 kb and normalized to ROT 5. This is a
        primary library enriched for full-length clones and
        constructed using the Cap-trapper method (Carninci, in
        preparation). Library constructed by M. Brownstein
        (NIH/NHGRI, National Institutes of Health). Note: this is
        a NIH_MGC Library."

ORIGIN
  Query Match      87.2%; Score 21.8; DB 4; Length 863;
  Best Local Similarity 68.0%; Pred. No. 37;
  Matches 17; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGAUUCCAGAUAGCC 25
  |||:|||||:|||||:|||||
Db 405 CAACUUCAGAUUCCAGAUAGCC 381

RESULT 10
  LOCUS
  DEFINITION
    u05b10.y1 Sugano mouse liver mlia Mus musculus cDNA clone
    IMAGE:1891003 5' similar to TR:Q63765 Q63765 RAT Cl-13 GENE
    PRODUCT. :, mRNA sequence.
  ACCESSION
    AI225530
  VERSION
    AI225530.1 GI:3808583
  KEYWORDS
    EST.
  SOURCE
    Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE
    1 (bases 1 to 432)
    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
    Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
    Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
    Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
    Waterston,R.
  TITLE
    The WashU-HHMI Mouse EST Project
  JOURNAL
    Unpublished (1996)
  COMMENT
    Contact: Marra M/Mouse EST Project
    WashU-HHMI Mouse EST Project
    Washington University School of MedicineP
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: mouseest@watson.wustl.edu
    This clone is available royalty-free through LLNL; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    MGI:975327
    Seq primer: custom primer used
    High quality sequence stop: 425.
    Location/Qualifiers
      1..432
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL"
        /db_xref="taxon:10090"
        /clone="IMAGE:1891003"
        /sex="female"
        /dev_stage="adult"

FEATURES
  source
    High quality sequence stop: 689.
    Location/Qualifiers
      1..863
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:5313024"
        /tissue_type="hypothalamus"
        /lab_host="DH10B"
        /clone_lib="NIH MGC 96"
        /notes="Organ: Brain; Vector: pBluescriptR (modified
        pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
        (ctcag); Oligo-dT primed using primer
        5'-TTTTTTTTTTTTTNN-3', size-selected for average
        insert size 2.3 kb and normalized to ROT 5. This is a
        primary library enriched for full-length clones and
        constructed using the Cap-trapper method (Carninci, in
        preparation). Library constructed by M. Brownstein
        (NIH/NHGRI, National Institutes of Health). Note: this is
        a NIH_MGC Library."

ORIGIN
  Query Match      83.2%; Score 20.8; DB 1; Length 432;
  Best Local Similarity 64.0%; Pred. No. 95;
  Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACUUCAGAUUCCAGAUAGCC 25
  |||:|||||:|||||:|||||
Db 381 CAACUUCAGAUUCCAGAUAGCC 357

RESULT 11
  LOCUS
  DEFINITION
    AZ513867 515 bp DNA linear GSS 05-OCT-2000
    clone UUGC1M0360J08 F, genomic survey sequence.
  ACCESSION
    AZ513867
  VERSION
    AZ513867.1 GI:10695183
  KEYWORDS
    GSS.
  SOURCE
    Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE
    1 (bases 1 to 515)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weise,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunne@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0360 row: J column: 08
    Seq primer: CGTTGTAACGACGCCAGT
    Claes: plasmid ends
    High quality sequence stop: 515.
    Location/Qualifiers
      1..515
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0360J08"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resources
        (http://www.jax.org/resources/documents/dnares/). The DNA

```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 83.2%; Score 20.8; DB 8; Length 515;
Best Local Similarity 70.8%; Pred. No. 99;
Matches 17; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUACAGGAUCCAGAUAGCCC 25

Db 514 AACATCAGGATTCAGGTATGCC 491

RESULT 12

AV726731/c 673 bp mRNA linear EST 17-OCT-2000

LOCUS AV726731 HTC Homo sapiens cDNA clone HTCENF02 5', mRNA sequence.

ACCESSION AV726731

VERSION AV726731.1 GI:10836152

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 673)

AUTHORS

Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z., and Han, Z.

Homo sapiens cDNA HTC clones

Unpublished (2000)

TITLE

Contact: Zeguaguan

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919 (ex. 45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

source

1. .673
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HTCENF02"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="HTC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 83.2%; Score 20.8; DB 1; Length 673;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 16; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUACAGGAUCCAGAUAGCCC 25

Db 34 AACCTTAAGATTCAGATATGCC 11

RESULT 13

LOCUS BF791086/c

DEFINITION

BF791086 698 bp mRNA linear EST 12-JAN-2001
602551165F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338353 5', mRNA sequence.

ACCESSION BF791086

VERSION BF791086.1 GI:12096140

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 698)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLC1214 row: b column: 18

High quality sequence stop: 162.

FEATURES

source

1. .698
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4338353"
/lab_host="NIH MGC 81"
/clone_lib="NIH MGC 81"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggccatgatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 83.2%; Score 20.8; DB 2; Length 698;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 16; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUACAGGAUCCAGAUAGCCC 25

Db 110 AACCTCAGATTCAGATATGCC 87

RESULT 14

LOCUS AA193133/c

DEFINITION

AA193133 473 bp mRNA linear EST 12-MAR-1998
zq13c03.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:629572 5' similar to TR:G307311 G307311 H1STONE H4. ;, mRNA sequence.

ACCESSION AA193133

VERSION AA193133.1 GI:1782528

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 473)

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:52:26 ; Search time 90.2027 Seconds
(without alignments)
453.500 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCUTS_COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.2	76.8	601	4	US-09-949-016-44986
C 2	19.2	76.8	601	4	US-09-949-016-44987
C 3	19.2	76.8	601	4	US-09-949-016-44988
C 4	19.2	76.8	165651	4	US-09-949-016-13032
C 5	18.8	75.2	237241	4	US-09-949-016-16101
C 6	18.6	74.4	1830121	4	US-09-557-8884-1
C 7	18.6	74.4	1830121	4	US-09-643-990A-1
C 8	18.4	73.6	8473	3	US-09-172-422-2
C 9	17.4	69.6	66247	4	US-09-949-016-16009
C 10	17.4	69.6	128723	4	US-09-949-016-17533
C 11	17.2	68.8	15572	4	US-09-424-783-1
C 12	17.2	68.8	192700	4	US-09-949-016-11820
C 13	17.2	68.8	192704	4	US-09-949-016-17182
C 14	17	68.0	1742	4	US-09-205-258-49
C 15	17	68.0	38844	3	US-09-734-673-3
C 16	17	68.0	44393	4	US-09-949-016-14944
C 17	17	68.0	44393	4	US-09-949-016-14945
C 18	17	68.0	44393	4	US-09-949-016-14946
C 19	17	68.0	44393	4	US-09-949-016-16911
C 20	17	68.0	114793	4	US-10-148-806-3
C 21	17	68.0	524032	4	US-09-949-016-16928
C 22	17	68.0	524032	4	US-09-949-016-16929
C 23	17	68.0	524032	4	US-09-949-016-16930
C 24	17	68.0	524032	4	US-09-949-016-16931
C 25	17	68.0	529885	4	US-09-949-016-14340
C 26	17	68.0	529885	4	US-09-949-016-14341
C 27	17	68.0	529885	4	US-09-949-016-14342

C 28	17	68.0	529885	4	US-09-949-016-14343	Sequence 14343, A
C 29	17	68.0	529885	4	US-09-949-016-14344	Sequence 14344, A
C 30	17	68.0	529885	4	US-09-949-016-14345	Sequence 14345, A
C 31	17	68.0	529885	4	US-09-949-016-14346	Sequence 14346, A
C 32	17	68.0	529885	4	US-09-949-016-14347	Sequence 14347, A
C 33	16.8	67.2	465	4	US-09-640-211A-1911	Sequence 1911, Ap
C 34	16.8	67.2	954	4	US-09-328-352-3988	Sequence 3988, Ap
C 35	16.8	67.2	4305	4	US-09-645-593-1	Sequence 1, Appli
C 36	16.8	67.2	137949	4	US-09-949-016-12196	Sequence 12196, A
C 37	16.8	67.2	137956	4	US-09-949-016-17260	Sequence 17260, A
C 38	16.6	66.4	601	4	US-09-949-016-182462	Sequence 182462, A
C 39	16.6	66.4	601	4	US-09-949-016-182463	Sequence 182463, A
C 40	16.6	66.4	601	4	US-09-949-016-182464	Sequence 182464, A
C 41	16.6	66.4	601	4	US-09-949-016-182582	Sequence 182582, A
C 42	16.6	66.4	601	4	US-09-949-016-182583	Sequence 182583, A
C 43	16.6	66.4	601	4	US-09-949-016-182584	Sequence 182584, A
C 44	16.6	66.4	1651	4	US-09-270-767-29747	Sequence 29747, A
C 45	16.6	66.4	1761	4	US-09-270-767-13725	Sequence 13725, A

ALIGNMENTS

RESULT 1

US-09-949-016-44986/c
; Sequence 44986, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44986
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44986

Query Match 76.8%; Score 19.2; DB 4; Length 601;
Best Local Similarity 66.7%; Pred. No. 9.8;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACUUCAGGUAUCCAGUAUGCCC 25

Db 491 AATCCAGGATTCAGTATGCC 468

RESULT 2

US-09-949-016-44987/c
; Sequence 44987, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44987
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44987

Query Match          76.8%; Score 19.2; DB 4; Length 601;
Best Local Similarity 66.7%; Pred. No. 9.8;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCCC 25
   || : ||||| : ||||| : |||||
Db 368 AATTCAGGATTCAGCTATGCC 345

RESULT 3
US-09-949-016-44988/c
; Sequence 44988, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44988
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44988

Query Match          76.8%; Score 19.2; DB 4; Length 601;
Best Local Similarity 66.7%; Pred. No. 9.8;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCCC 25
   || : ||||| : ||||| : |||||
Db 298 AATTCAGGATTCAGCTATGCC 275

RESULT 4
US-09-949-016-13032/c
; Sequence 13032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13032
; LENGTH: 165651
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13032

Query Match          76.8%; Score 19.2; DB 4; Length 165651;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCCC 25
   || : ||||| : ||||| : |||||
Db 13590 AATTCAGGATTCAGCTATGCC 13567

RESULT 5
US-09-949-016-16101/c
; Sequence 16101, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16101
; LENGTH: 237241
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16101

Query Match          75.2%; Score 18.8; DB 4; Length 237241;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCGAGAUAG 22
   ||||| : ||||| : ||||| : |||||
Db 189288 CAATTCAGGATTCAGGTATG 189267

RESULT 6
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
```

```

; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 74.4%; Score 18.6; DB 4; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 74;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUUGCCC 25
Db 1071778 CACTTCAGGATGCCCTTTATGCC 1071754

RESULT 7
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
;
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-544-776-4-1

Query Match 74.4%; Score 18.6; DB 4; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 74;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUUGCCC 25
Db 1071778 CACTTCAGGATGCCCTTTATGCC 1071754

RESULT 8
US-09-172-422-2/c
; Sequence 2, Application US/09172422A
; Patent No. 6300485
; GENERAL INFORMATION:
; APPLICANT: Adams, Arwen E.
; APPLICANT: Chiu, Choi Ying
; APPLICANT: Duhl, David
; APPLICANT: Gorman, Susan W.
; APPLICANT: Leng, Song
; APPLICANT: Sheffield, Val
; APPLICANT: Welch, Juliet
; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
; CHANNEL-15 (CNCG-15) POLYNUCLEOTIDES, POLYPEPTIDES,
; AND USES THEREOF
; FILE REFERENCE: 200130.442
; CURRENT APPLICATION NUMBER: US/09/172.422A
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 8473
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-172-422-2

Query Match 73.6%; Score 18.4; DB 3; Length 8473;
Best Local Similarity 65.0%; Pred. No. 38;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUU 21
Db 1595 AACTTCAGGATACAGATAT 1576

RESULT 9
US-09-949-016-16009/c
; Sequence 16009, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 16009
; LENGTH: 66247
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16009

Query Match 69.6%; Score 17.4; DB 4; Length 66247;
Best Local Similarity 68.4%; Pred. No. 1.7e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAU 19
||||:||||:||||:
DB 60760 CAACTTAGGATCCAGAT 60742

RESULT 10
US-09-949-016-17533/c
; Sequence 17533, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 17533
; LENGTH: 128723
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17533

Query Match 69.6%; Score 17.4; DB 4; Length 128723;
Best Local Similarity 73.7%; Pred. No. 1.9e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAU 20
||||:||||:||||:
DB 108647 AACTTCAGGATCCAGAA 108629

RESULT 11
US-09-424-783-1/c
; Sequence 1, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: DE 197 22 317.6
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1

; LENGTH: 15572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-424-783-1

Query Match 68.8%; Score 17.2; DB 4; Length 15572;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAU 22
||||:||||:||||:
DB 13920 CAACTCCAGCTCCAGATG 13899

RESULT 12
US-09-949-016-11820
; Sequence 11820, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11820
; LENGTH: 192700
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11820

Query Match 68.8%; Score 17.2; DB 4; Length 192700;
Best Local Similarity 63.6%; Pred. No. 2.5e+02;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAU 22
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DB 85389 CCATTCAGGAATCCAGATG 85410

RESULT 13
US-09-949-016-17182
; Sequence 17182, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 17182
; LENGTH: 192704
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17182

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Query Match      68.8%; Score 17.2; DB 4; Length 192704;
Best Local Similarity 63.8%; Pred. No. 2.5e+02;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 CAACUUCAGAGUCCAGAUUG 22
Db      85389 CCATTTCAGGATCCAGATG 85410

RESULT 14
US-09-205-258-49/c
; Sequence 49, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
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; EARLIER APPLICATION NUMBER: 60/048,882
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
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; EARLIER APPLICATION NUMBER: 60/048,916
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; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06

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; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: SITE
; LOCATION: (570)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-49

Query Match      68.0%; Score 17; DB 4; Length 1742;
Best Local Similarity 68.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 CAACUUCAGAGUCCAGAUUGCCC 25
Db      699 CAATGCAGGCTTCAGGAGGCC 675

RESULT 15
US-09-734-675-3
; Sequence 3, Application US/09734675
; Patent No. 6365391
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO00862
; CURRENT APPLICATION NUMBER: US/09/734,675
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 38844
; TYPE: DNA
; ORGANISM: Human
US-09-734-675-3

Query Match      68.0%; Score 17; DB 3; Length 38844;
Best Local Similarity 64.0%; Pred. No. 2.4e+02;

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Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAACTUCAGGAUCCAGAUUGGCC 25
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Db 14970 CAACTACAAAATTCTAGAAATGCC 14994

Search completed: July 30, 2005, 15:05:43
Job time : 98.2027 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:00:21 ; Search time 702.486 Seconds
(without alignments)
1655.441 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 auuccaccagucgucagauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0 .

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
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11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 2	24	100.0	170	6	CQ712889	Sequence
C 3	24	100.0	191	6	CQ683836	Sequence
C 4	24	100.0	207	11	G05614	human STS W
C 5	24	100.0	370	6	CQ709205	Sequence
C 6	24	100.0	468	6	CQ686446	Sequence
C 7	24	100.0	496	6	AX895341	Sequence
C 8	24	100.0	496	6	BD030874	Sequence
C 9	24	100.0	536	6	CQ781164	Sequence
C 10	24	100.0	536	6	BD125873	Sequence
C 11	24	100.0	559	6	CQ782338	Sequence
C 12	24	100.0	559	6	BD127047	Sequence
C 13	24	100.0	1079	9	BC007109	Sequence
C 14	24	100.0	1206	9	AK172726	Sequence
C 15	24	100.0	1213	6	BD194907	Sequence
C 16	24	100.0	1213	6	CQ855235	Sequence
C 17	24	100.0	1466	9	BC071848	Sequence
C 18	24	100.0	1610	6	BD231889	Sequence
C 19	24	100.0	1617	9	AF087901	Sequence

C 20	24	100.0	1619	9	AK129806	Homo sapi
C 21	24	100.0	1691	9	AF132048	Homo sapi
C 22	24	100.0	1694	6	CQ783030	Sequence
C 23	24	100.0	1694	6	BD127437	Primer fo
C 24	24	100.0	1694	9	AK075039	Homo sapi
C 25	24	100.0	1698	9	BC014366	Homo sapi
C 26	24	100.0	1700	9	AF177332	Homo sapi
C 27	24	100.0	1728	9	BC068991	Homo sapi
C 28	24	100.0	1784	9	BC016185	Homo sapi
C 29	24	100.0	1800	9	AY102276	Homo sapi
C 30	24	100.0	2162	9	AB049853	Macaca fa
C 31	24	100.0	2235	9	AF148538	Homo sapi
C 32	24	100.0	2332	9	AY102277	Homo sapi
C 33	24	100.0	2386	6	BD190738	Secreted
C 34	24	100.0	2386	6	AX099401	Sequence
C 35	24	100.0	2389	9	AY102278	Homo sapi
C 36	24	100.0	3491	9	AF333336	Homo sapi
C 37	24	100.0	3919	6	CQ829486	Sequence
C 38	24	100.0	4053	6	AX195249	Sequence
C 39	24	100.0	4053	9	AB020693	Homo sapi
C 40	24	100.0	4060	9	AY123250	Homo sapi
C 41	24	100.0	4070	9	AY123249	Homo sapi
C 42	24	100.0	4093	6	BD270070	Secreted
C 43	24	100.0	4102	9	AY123245	Homo sapi
C 44	24	100.0	4109	9	AY123248	Homo sapi
C 45	24	100.0	4123	9	AY123247	Homo sapi

ALIGNMENTS

RESULT 1	CQ688348	Sequence	33274	from Patent WO02070737.	144 bp	DNA	linear	PAT 03-FEB-2004
LOCUS	CQ688348	Sequence	33274	from Patent WO02070737.	144 bp	DNA	linear	PAT 03-FEB-2004
DEFINITION	CQ688348	Sequence	33274	from Patent WO02070737.	144 bp	DNA	linear	PAT 03-FEB-2004
ACCESSION	CQ688348	Sequence	33274	from Patent WO02070737.	144 bp	DNA	linear	PAT 03-FEB-2004
VERSION	CQ688348.1	GI:42220578						
KEYWORDS								
SOURCE								
ORGANISM	Homo sapiens (human)							
REFERENCE	1							
AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.							
TITLE	Compositions and methods relating to osteoarthritis							
JOURNAL	Patent: WO 02070737-A 33274 12-SEP-2002;							
FEATURES	Chondrogene Inc. (CA)							
source	Location/Qualifiers							
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Best Local Similarity	79.2%;	Pred. No. 3.6;						
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QY	1	ATUCCACCAAGUCGUCGAGUAGGA	24					
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LOCUS	CQ712889/c	Sequence	57815	from Patent WO02070737.	170 bp	DNA	linear	PAT 03-FEB-2004
DEFINITION	CQ712889	Sequence	57815	from Patent WO02070737.	170 bp	DNA	linear	PAT 03-FEB-2004
ACCESSION	CQ712889	Sequence	57815	from Patent WO02070737.	170 bp	DNA	linear	PAT 03-FEB-2004
VERSION	CQ712889.1	GI:42273746						
KEYWORDS								
SOURCE								
ORGANISM	Homo sapiens (human)							
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 57815 12-SEP-2002;
Chondrogene Inc. (CA)

FEATURES

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1. .170
Location/Qualifiers
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ORIGIN

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Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGCGCUCAGAUAGGA 24

Db 97 ATTCACCAGTGCCTCAGATAGGA 74

RESULT 3

CQ683836/c
LOCUS CQ683836 191 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 28762 from Patent WO02070737.
ACCESSION CQ683836
VERSION CQ683836.1 GI:42207284

KEYWORDS

source Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 28762 12-SEP-2002;
Chondrogene Inc. (CA)

FEATURES

source
1. .191
Location/Qualifiers
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Best Local Similarity 79.2%; Pred. No. 3.4;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGCGCUCAGAUAGGA 24

Db 116 ATTCACCAGTGCCTCAGATAGGA 93

RESULT 4

G05614
LOCUS G05614 207 bp DNA linear STS 19-OCT-1995
DEFINITION human STS WI-6613, sequence tagged site.

ACCESSION

source G05614.1 GI:858859

VERSION

STG; STS sequence; primer; sequence tagged site.

KEYWORDS

source Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ORGANISM

Homo sapiens
1 (bases 1 to 207)
Hudson,I.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)

REFERENCE

AUTHORS Contact: Thomas Hudson
TITLE Whitehead Institute/MIT Center for Genome Research
JOURNAL Whitehead Institute/MIT Center for Genome Research
COMMENT

Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: TAGCTCCACCATCTCTGCAA

Primer B: GTCTTGACTGCCATGTGTCA

STS size: 175

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: each 4 nM

Tag Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCL: 10 mM

pH: 9.3

Prepared with primer pairs derived from Z38593 -- dbEST.

FEATURES

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Location/Qualifiers
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/db_xref="taxon:9606"

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CR from top of Chr2 linkage group"

STS

primer_bind 2. .176

primer_bind 2. .21

complement(156. .176)

ORIGIN

Query Match 100.0%; Score 24; DB 11; Length 207;
Best Local Similarity 79.2%; Pred. No. 3.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGCGCUCAGAUAGGA 24

Db 76 ATTCACCAGTGCCTCAGATAGGA 99

RESULT 5

CQ709205/c

LOCUS CQ709205 370 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 54131 from Patent WO02070737.

ACCESSION CQ709205

VERSION CQ709205.1 GI:42270021

KEYWORDS Homo sapiens (human)

source Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Liew,C.C., Marshall,W.E. and Zhang,H.

AUTHORS Compositions and methods relating to osteoarthritis

TITLE Patent: WO 02070737-A 54131 12-SEP-2002;

JOURNAL Chondrogene Inc. (CA)

FEATURES source

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Location/Qualifiers

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

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Db 76 ATTCCACCAGTGCCTCAGATAGGA 99

RESULT 10
LOCUS BD125873 536 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD125873
VERSION BD125873.1 GI:23220818
KEYWORDS JP 2002017375-A/1304.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 536)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/1304
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 536;
Best Local Similarity 79.2%; Pred. No. 2.8;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
LOCUS CO782338 559 bp DNA linear PAT 17-MAR-2004
DEFINITION Sequence 2478 from Patent EP1396543.
ACCESSION CO782338
VERSION CO782338.1 GI:45538394
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/1304
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
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Query Match 100.0%; Score 24; DB 6; Length 536;
Best Local Similarity 79.2%; Pred. No. 2.8;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGUCUCAGAUAGGA 24
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Db 76 ATTCCACCAGTGCCTCAGATAGGA 99

RESULT 12
LOCUS BD127047 559 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127047
VERSION BD127047.1 GI:23221992
KEYWORDS JP 2002017375-A/2478.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 559)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2478
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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FEATURES
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Best Local Similarity 79.2%; Pred. No. 2.7;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGUCUCAGAUAGGA 24
   |:|||||:~|:~|:~|:~|:~|:~|:~|
Db 76 ATTCCACCAGTGCCTCAGATAGGA 99

RESULT 13
LOCUS BC007109/c 1079 bp mRNA linear PRI 29-JUN-2004

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TITLE Primers for synthesizing full length cDNA clones and their use
JOURNAL Patent: EP 1396543-A 2478 10-MAR-2004;
Research Association for Biotechnology (JP)
FEATURES
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1..559
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/mol_type='unassigned DNA'
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ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 559;
Best Local Similarity 79.2%; Pred. No. 2.7;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGUCUCAGAUAGGA 24
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Db 76 ATTCCACCAGTGCCTCAGATAGGA 99

RESULT 12
LOCUS BD127047 559 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127047
VERSION BD127047.1 GI:23221992
KEYWORDS JP 2002017375-A/2478.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 559)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2478
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 559;
Best Local Similarity 79.2%; Pred. No. 2.7;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGUCUCAGAUAGGA 24
   |:|||||:~|:~|:~|:~|:~|:~|:~|
Db 76 ATTCCACCAGTGCCTCAGATAGGA 99

RESULT 13
LOCUS BC007109/c 1079 bp mRNA linear PRI 29-JUN-2004

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Search completed: July 30, 2005, 12:54:29
Job time : 703.486 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:32:26 ; Search time 296.108 Seconds
(without alignments)
479.804 Million cell updates/sec

Title: US-09-544-776-5
Perfect score: 24
Sequence: 1 auuccaccagucucagauagga 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2002bs:*

8: Geneseq2003as:*

9: Geneseq2003bs:*

10: Geneseq2003cs:*

11: Geneseq2003ds:*

12: Geneseq2004as:*

13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	3 AAC64409	Rac64409 Human Nog
2	24	100.0	496	3 AAC07129	Aac07129 Human sec
3	24	100.0	536	4 AAC92844	Aac92844 Human CDN
4	24	100.0	536	12 ADL29271	Adl29271 3' end of
5	24	100.0	559	4 AAK94018	Aak94018 Human CDN
6	24	100.0	559	12 ADL30445	Adl30445 3' end of
7	24	100.0	972	10 ADG63407	Adg63407 Partial h
8	24	100.0	1213	2 AAX04379	Aax04379 Human sec
9	24	100.0	1610	3 AAZ36230	Aaz36230 cDNA enco
10	24	100.0	1683	4 AAD08386	Aad08386 Human sec
11	24	100.0	1694	4 AAK94408	Aak94408 Human ful
12	24	100.0	1694	12 ADL31137	Adl31137 Full leng
13	24	100.0	1758	4 AAF32725	Aaf32725 Human sec
14	24	100.0	1785	12 ADKL4166	Adkl4166 Human aut
15	24	100.0	2235	6 ABV94681	Abv94681 Human pan
16	24	100.0	2240	3 AAC64406	Aac64406 Human Nog
17	24	100.0	2386	2 AAV30920	Aav30920 Human sec
18	24	100.0	2386	5 AAF98399	Aaf98399 Human CDN
19	24	100.0	2512	12 ADQ15813	Adq15813 4 synthes
20	24	100.0	3919	12 ADP45550	Adp45550 Human Nog

C 21	24	100.0	4053	4 AAS09453	Ras09453 Human CDN
C 22	24	100.0	4053	9 ACC81048	Acc81048 Human Nog
C 23	24	100.0	4053	12 ADP13574	Adp13574 Renal cel
C 24	24	100.0	4093	3 AAA23454	Aaa23454 cDNA enco
C 25	24	100.0	4632	6 ABV94680	Abv94680 Human pan
C 26	24	100.0	4632	10 ADG32772	Adg32772 Human DNA
C 27	24	100.0	4698	8 ABX34563	Abx34563 Human mdd
C 28	24	100.0	4710	4 AAL04697	Aal04697 Human rep
C 29	24	100.0	4710	4 ABL97604	AbL97604 Human tes
C 30	24	100.0	4789	13 ADR83534	Adr83534 Human ret
C 31	24	100.0	4822	6 ABS70449	Abs70449 Human bon
C 32	22	91.7	25	12 ADP17627	Adp17627 Renal cel
C 33	22	91.7	211	2 AAX23499	Aax23499 Human neu
C 34	22	91.7	360	5 AAS29079	Aas29079 cDNA enco
C 35	22	91.7	360	6 ABS68219	Abs68219 cDNA enco
C 36	22	91.7	360	10 ADC25213	Adc25213 Human CDN
C 37	22	91.7	377	5 AAS29151	Aas29151 cDNA enco
C 38	22	91.7	377	6 ABS68291	Abs68291 cDNA enco
C 39	22	91.7	377	10 ADC25285	Adc25285 Human CDN
C 40	22	91.7	385	4 AAH72193	Aah72193 Human cer
C 41	22	91.7	410	9 ACH35051	Ach35051 Human end
C 42	22	91.7	510	4 AAH69329	Aah69329 Human cer
C 43	22	91.7	602	5 ABV49730	Abv49730 Human pro
C 44	22	91.7	633	5 ABV19969	Abv19969 Human pro
C 45	22	91.7	702	4 AAH71132	Aah71132 Human cer

ALIGNMENTS

RESULT 1
AAC64409
ID AAC64409 standard; RNA; 24 BP.

XX AAC64409;

DT 08-FEB-2001 (first entry)

XX Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:5.

XX Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
stres-phosphorylated endoplasmic reticulum protein; cytosstatic;
gene therapy; cell growth; cellular stress response; neuron growth;
KW regulator of oxidative stress; inhibitor of neurite outgrowth;
KW axon regeneration; diagnosis; cancer; identification; antisense;
phosphorothioate; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH modified_base 1..24
FT /*tag= a
FT /note= "phosphorothioate linkages"

XX WO2000060083-A1.

XX 12-OCT-2000.

XX 07-APR-2000; 2000WO-US009383.

XX 08-APR-1999; 99US-0128372P.

XX 21-JUN-1999; 99US-0140331P.

XX (CHIR) CHIRON CORP.

XX Wei D, Halenbeck R, Williams LT;

XX WPI; 2000-665007/64.

XX Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic

CC reticulum protein, designated Nogo B. Nogo B has cytosolic activity and

CC is a modulator of the storage and exchange of calcium, cell growth and

CC cellular stress response. It can: regulate oxidative stress; inhibit

CC neurite outgrowth, neuron growth and axon regeneration. Nogo B

CC polypeptides and polynucleotides are useful for modulating stress levels

CC and cellular stress-response, cell growth and viability, diagnosis and

CC treatment of cancer, malignant growth and other Nogo B related diseases.

CC Nogo B polypeptides are also useful to screen combinatorial libraries to

CC identify agonist or antagonist. Antibodies against Nogo B polypeptides

CC are useful for affinity chromatography and distinguishing Nogo B

CC polypeptides. The present sequence represents a human Nogo B

XX phosphorothioate antisense oligonucleotide from the present invention

XX

SQ Sequence 24 BP; 7 A; 7 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Gaps 0;

Matches 24; Conservative 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGUGCCUCAGAUAGGA 24
|||||

Db 1 AUUCCACCAGUGCCUCAGAUAGGA 24
|||||

RESULT 2

ID AAC07129/c

XX AAC07129 standard; cDNA; 496 BP.

AC AAC07129;

XX

DT 06-OCT-2000 (first entry)

XX

DE Human secreted protein 5' EST, SEQ ID NO: 11204.

XX

DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping; ss.

XX

OS Homo sapiens.

XX

XX EP1033401-A2.

PN

XX

PD 06-SEP-2000.

XX

XX 21-FEB-2000; 2000EP-00200610.

PF

XX 26-FEB-1999; 99US-0122487P.

PR

XX (GEST) GENSET.

PA

XX Dumas Milne Edwards J, Duclert A, Giordano J;

PI

XX WPI; 2000-500381/45.

DR

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PT

XX Claim 1; SEQ ID NO 11204; 71pp + Sequence Listing; English.

PS

XX The present sequence is one of a large number of 5' ESTs derived from

CC mRNAs encoding secreted proteins. No ORF has yet been conclusively

CC identified within the present sequence. The 5' ESTs were prepared from

CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST

CC sequences usually correspond mainly to the 3' untranslated region (UTR)

CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer

CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'

CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used

CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in

CC

CC diagnostic, forensic, gene therapy and chromosome mapping procedures.

CC They are used to obtain upstream regulatory sequences and to design

CC expression and secretion vectors

XX

SQ Sequence 496 BP; 156 A; 77 C; 104 G; 158 T; 0 U; 1 Other;

Query Match 100.0%; Score 24; DB 3; Length 496;

Best Local Similarity 79.2%; Pred. No. 0.19; Mismatches 0; Gaps 0;

Matches 19; Conservative 5; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGUGCCUCAGAUAGGA 24
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Db 410 ATTCCACCAGTGCCTCAGATAGGA 387
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RESULT 3

AAK92844

ID AAK92844 standard; cDNA; 536 BP.

XX

AC AAK92844;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human cDNA 3'-end sequence, SEQ ID NO: 1304.

XX

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

KW

XX Homo sapiens.

OS

XX EP1130094-A2.

PN

XX

PD 05-SEP-2001.

XX

XX 07-JUL-2000; 2000EP-00114089.

PF

XX 08-JUL-1999; 99JP-00194486.

PR

XX 11-JAN-2000; 2000JP-00118774.

PR

XX 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

XX WPI; 2001-524255/58.

DR

XX 830 Primers useful for synthesizing full length cDNA clones and their use

PT in genetic manipulation.

PT

XX Claim 3; SEQ ID NO 1304; 1380pp + Sequence Listing; English.

PS

XX The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been isolated

CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

CC been determined. Primers for synthesizing the full length cDNA are useful

CC for clarifying the function of the protein encoded by the cDNA. The full

CC length clones were obtained by construction of full length enriched cDNA

CC libraries that were synthesised by the oligo-capping method. The primers

CC enable the production of the full length cDNA easily without any special

CC methods. The present sequence is the nucleotide sequence of the 3'-end of

CC a cDNA provided in the invention. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in CD-

CC ROM format directly from EPO

XX

SQ Sequence 536 BP; 169 A; 120 C; 92 G; 148 T; 0 U; 7 Other;

Query Match 100.0%; Score 24; DB 4; Length 536;

Best Local Similarity 79.2%; Pred. No. 0.2; Mismatches 0; Gaps 0;

Matches 19; Conservative 5; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGUGCCUCAGAUAGGA 24
|:|||||:|||||:|||||

Db 76 ATTCCACCAGTGCCTCAGATAGGA 99
|:|||||:|||||:|||||


```

RESULT 4
ADL29271
ID ADL29271 standard; cDNA; 536 BP.
XX AC
XX AC ADL29271;
XX DT
XX DT 20-MAY-2004 (first entry)
XX DE
XX DE 3' end of a human cDNA molecule SeqID 1304.
XX KW human; medicine; signal transduction; glycoprotein; transcription;
XX KW oligo-capping method; ss.
XX OS Homo sapiens.
XX PN
XX PN EPI1396543-A2.
XX PD
XX PD 10-MAR-2004.
XX PF
XX PF 07-JUL-2000; 2003EP-00025638.
XX PR
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183865.
XX PR 07-JUL-2000; 2000EP-00114089.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX DR
XX DR WPI; 2004-204755/20.
XX PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX PT length human cDNAs.
XX PS Disclosure; SEQ ID NO 1304; 1340pp; English.
XX SQ
XX This invention relates to a novel primers useful for synthesizing full
XX length cDNA molecules that encode human proteins. Specifically, it refers
XX to secretory or membrane proteins that are potential therapeutic agents/
XX target molecules in the field of medicine, and in particular genes
XX encoding proteins that are associated with signal transduction,
XX glycoproteins and transcription. The present invention describes a method
XX for efficiently cloning a full length human cDNA from both the 5' and 3'
XX ends using the oligo-capping method. This polynucleotide sequence is the
XX 3' end of a full length human cDNA sequence of the invention.
XX SQ Sequence 536 BP; 169 A; 120 C; 92 G; 148 T; 0 U; 7 Other;
XX Query Match 100.0%; Score 24; DB 12; Length 536;
XX Best Local Similarity 79.2%; Pred. No. 0.2;
XX Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 AUUCCACCAGGCGCCUCAGAUAGGA 24
Db ::::::::::::::::::::::::::::
76 ATTCACCAGTGCTCAGATAGGA 99
RESULT 5
AAK94018
ID AAK94018 standard; cDNA; 559 BP.
XX AC
XX AC AAK94018;
XX DT
XX DT 06-NOV-2001 (first entry)
XX DE
XX DE Human cDNA clone representative sequence, SEQ ID NO: 2478.
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX KW

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OS Homo sapiens.
XX PN
XX PN EPI130094-A2.
XX PD
XX PD 05-SEP-2001.
XX PF
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX PI
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX DR
XX DR WPI; 2001-524255/58.
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX PT in genetic manipulation.
XX PS Example 11; SEQ ID NO 2478; 1380pp + Sequence Listing; English.
XX SQ
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesizing the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence was used as the representative sequence
XX from a human clone which was used in homology searches to identify the
XX clone. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in CD-ROM format directly from
XX EPO
XX SQ Sequence 559 BP; 178 A; 129 C; 94 G; 152 T; 0 U; 6 Other;
XX Query Match 100.0%; Score 24; DB 4; Length 559;
XX Best Local Similarity 79.2%; Pred. No. 0.2;
XX Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 AUUCCACCAGGCGCCUCAGAUAGGA 24
Db ::::::::::::::::::::::::::::::
76 ATTCACCAGTGCTCAGATAGGA 99
RESULT 6
ADL30445
ID ADL30445 standard; cDNA; 559 BP.
XX AC
XX AC ADL30445;
XX DT
XX DT 20-MAY-2004 (first entry)
XX DE
XX DE 3' end of a representative human cDNA cluster SeqID 2478.
XX KW human; medicine; signal transduction; glycoprotein; transcription;
XX KW oligo-capping method; ss.
XX OS Homo sapiens.
XX PN
XX PN EPI1396543-A2.
XX PD
XX PD 10-MAR-2004.
XX PF
XX PF 07-JUL-2000; 2003EP-00025638.
XX PR
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183865.

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PR 07-JUL-2000; 2000EP-00114089.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2004-204755/20.
XX
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX length human cDNAs.
XX
XX Example 18; SEQ ID NO 2478; 1340pp; English.
XX
XX This invention relates to a novel primers useful for synthesising full
XX length cDNA molecules that encode human proteins. Specifically, it refers
XX to secretory or membrane proteins that are potential therapeutic agents/
XX target molecules in the field of medicine, and in particular genes
XX encoding proteins that are associated with signal transduction.
XX glycoproteins and transcription. The present invention describes a method
XX for efficiently cloning a full length human cDNA from both the 5' and 3'
XX ends using the oligo-capping method. This polynucleotide sequence is the
XX 3' end of a representative human DNA cluster of the invention.
XX
XX Sequence 559 BP; 178 A; 129 C; 94 G; 152 T; 0 U; 6 Other;
SQ

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Query Match 100.0%; Score 24; DB 12; Length 559;
 Best Local Similarity 79.2%; Pred. No. 0.2;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AUUCCACCAGGCGCCUCAGAUAGGA 24
   |:|||||:|||||:|||||:|||||
DB 76 ATTCACCAGTGCCTCAGATAGGA 99

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RESULT 7
 ADG63407/c
 ID ADG63407 standard; cDNA; 972 BP.
 AC ADG63407;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Partial human Nogo cDNA.
 XX
 KW ss; human; neuropsychiatric disorder; Nogo polymorphism; Nogo;
 KW polymorphism; schizophrenia.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(244..249,ct)
 FT /*tag= a
 FT /note= "Deletion associated with CAA polymorphism"
 FT variation replace(725..729,cc)
 FT /*tag= b
 FT /note= "Polymorphism"
 XX
 PN US2003215868-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 15-MAY-2003; 2003US-00437931.
 XX
 PR 16-MAY-2002; 2002GB-00011212.
 XX
 PA (SEEM/) SEEMAN P.
 PA (NOVA/) NOVAK G.
 PA (TALL/) TALLERICO T.
 XX
 PI Seeman P, Novak G, Tallerico T;
 XX
 XX WPI; 2003-902032/82.
 DR

Determining susceptibility of patient to neuropsychiatric disorder, by obtaining sample from patient, and testing the sample for presence of polymorphism in Nogo gene.

Claim 2; SEQ ID NO 1; 12pp; English.

The invention relates to a method of determining the susceptibility of a patient to a neuropsychiatric disorder, comprising obtaining a sample from a patient, and testing the sample for the presence of a polymorphism in the Nogo gene, where the presence of a polymorphism indicates that the patient is susceptible to a neuropsychiatric disorder. The method is useful for determining the susceptibility of a patient to a neuropsychiatric disorder e.g. schizophrenia. The present sequence represents human Nogo partial cDNA.

Sequence 972 BP; 326 A; 155 C; 178 G; 313 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 10; Length 972;
 Best Local Similarity 79.2%; Pred. No. 0.22;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AUUCCACCAGGCGCCUCAGAUAGGA 24
   |:|||||:|||||:|||||:|||||
DB 265 ATTCACCAGTGCCTCAGATAGGA 242

```

RESULT 8
 AAX04379/c
 ID AAX04379 standard; DNA; 1213 BP.
 AC AAX04379;
 XX
 DT 13-APR-1999 (first entry)
 XX
 DE Human secreted protein gene 69 clone HAGFT48.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN WO9856804-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 11-JUN-1998; 98WO-US012125.
 XX
 PR 13-JUN-1997; 97US-0049547P.
 PR 13-JUN-1997; 97US-0049548P.
 PR 13-JUN-1997; 97US-0049549P.
 PR 13-JUN-1997; 97US-0049550P.
 PR 13-JUN-1997; 97US-0049566P.
 PR 13-JUN-1997; 97US-0049606P.
 PR 13-JUN-1997; 97US-0049607P.
 PR 13-JUN-1997; 97US-0049608P.
 PR 13-JUN-1997; 97US-0049609P.
 PR 13-JUN-1997; 97US-0049610P.
 PR 13-JUN-1997; 97US-0049611P.
 PR 13-JUN-1997; 97US-0050901P.
 PR 13-JUN-1997; 97US-0052989P.
 PR 08-JUL-1997; 97US-0051919P.
 PR 18-AUG-1997; 97US-0055984P.
 PR 12-SEP-1997; 97US-0058665P.
 PR 12-SEP-1997; 97US-0058668P.
 PR 12-SEP-1997; 97US-0058669P.
 PR 12-SEP-1997; 97US-0058750P.

XX DE Human secreted protein-encoding gene 42 cDNA clone HAGT48, SEQ ID NO:52.
 XX KW Human; secreted protein; proliferative disorder; cancer; tumour;
 XX KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 XX KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 XX KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 XX KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 XX KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 XX KW cardiovascular disorder; angioinetic disorder; kidney disorder;
 XX KW gastrointestinal disorder; pregnancy-related disorder;
 XX KW endocrine disorder; infection; wound healing; vulnertary; cell culture;
 XX KW chemotaxis; food additive; gene therapy; binding partner identification;
 XX KW ss.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT CDS 830..1192
 FT /*tag= a
 FT /product= "Human secreted protein precursor"
 FT /note= "CDS does not include start codon"
 FT /partial
 FT sig_peptide 830..898
 FT /*tag= b
 FT mat_peptide 899..1189
 FT /*tag= c
 FT /product= "Mature human secreted protein"
 XX WO200077022-A1.
 XX PD 21-DEC-2000.
 XX PF 01-JUN-2000; 2000WO-US015136.
 XX PF 11-JUN-1999; 99US-0138629P.
 XX PR (HUMA-) HUMAN GENOME SCI INC.
 XX PA Rosen CA, Ruben SM, Komatsoulis GA;
 XX PI WPI, 2001-367020/38.
 XX DR P-PSDB; AAE03939.
 XX DR Nucleic acids encoding 50 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's
 PT disease, botulism, cancers and Scimitar syndrome.
 XX Claim 1; Page 520; 614pp; English.
 XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
 CC protein genes and AAE03898-AAE03947 represent the proteins they encode.
 CC AAE03948-AAE03996 represent human secreted protein fragments or variants.
 CC The genes and their secreted proteins are useful for preventing, treating
 CC or ameliorating medical conditions, e.g. by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 50 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumours, foetal and developmental abnormalities,
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or

CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
 CC present sequence represents a human secreted protein-encoding cDNA of the
 XX invention
 SQ Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;
 Query Match 100.0%; Score 24; DB 4; Length 1683;
 Best Local Similarity 79.2%; Pred. NO. 0.23;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATCCACCAAGGCGCCAGCAUAGGA 24
 Db 1549 ATTCCACCAAGGCGCCAGCAUAGGA 1526
 RESULT 11
 AAK94408/c
 ID AAK94408 standard; cDNA; 1694 BP.
 XX AAK94408;
 AC
 XX 06-NOV-2001 (first entry)
 DT Human full-length cDNA, SEQ ID NO: 3170.
 XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
 KW Homo sapiens.
 OS
 XX EP1130094-A2.
 FN
 XX 05-SEP-2001.
 PD
 XX 07-JUL-2000; 2000EP-00114089.
 PF
 XX 08-JUL-1999; 99JP-00194486.
 PR
 XX 11-JAN-2000; 2000JP-00118774.
 PR
 XX 02-MAY-2000; 2000JP-00183765.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI; 2001-524255/58.
 DR P-PSDB; AAM93484.
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PS Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.
 XX The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a full length human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in CD-ROM format directly
 CC from EPO
 XX Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 24; DB 4; Length 1694;
 Best Local Similarity 79.2%; Pred. NO. 0.23;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCGCTCAGATAGGA 24
 Db 1619 ATTCACACGAGGCGCTCAGATAGGA 1596

RESULT 12
 ADL31137/c
 ID ADL31137 standard; cDNA; 1694 BP.
 AC ADL31137;
 DT 20-MAY-2004 (first entry)
 XX Full length human cDNA clone SeqID 3170.
 DE human; medicine; signal transduction; glycoprotein; transcription;
 KW oligo-capping method; ss; gene.
 KW Homo sapiens.
 OS
 PN EPI396543-A2.
 XX
 XX 10-MAR-2004.
 XX
 XX 07-JUL-2000; 2003EP-00025638.
 XX
 XX 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183865.
 PR 07-JUL-2000; 2000EP-00114089.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2004-204755/20.
 DR P-PSDB; ADL31138.
 XX
 XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
 PT length human cDNAs.
 XX
 PS Example 1; SEQ ID NO 3170; 1340pp; English.
 XX
 XX This invention relates to a novel primers useful for synthesizing full
 CC length cDNA molecules that encode human proteins. Specifically, it refers
 CC to secretory or membrane proteins that are potential therapeutic agents/
 CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3',
 CC ends using the oligo-capping method. This polynucleotide sequence is a
 CC full length human cDNA clone of the invention.
 XX
 SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 12; Length 1694;
 Best Local Similarity 79.2%; Pred. No. 0.23;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCGCTCAGATAGGA 24
 Db 1619 ATTCACACGAGGCGCTCAGATAGGA 1596

RESULT 13
 AAF32725
 ID AAF32725 standard; cDNA; 1758 BP.
 XX
 AC AAF32725;
 XX
 DT 23-MAR-2001 (first entry)

XX Human secreted protein gene 27 SEQ ID NO:37.
 DE Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 KW cerebroprotective; neutropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; cerebral ischaemia; infection;
 KW angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;
 KW ocular disorder; corneal infection; wound healing; food additive;
 KW preservative; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200077255-A1.
 PN
 XX 21-DEC-2000.
 PD
 XX
 XX 01-JUN-2000; 2000WO-US014926.
 PF
 XX
 XX 11-JUN-1999; 99US-0138628P.
 PR
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM, Komatsoulis GA;
 PI
 XX WPI; 2001-025337/03.
 DR P-PSDB; AAB64448.
 XX
 XX Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 PT
 XX
 PS Claim 1; Page 495; 593pp; English.
 XX
 XX The polynucleotide sequences given in AAF32699 to AAF32747 encode the
 CC human secreted proteins given in AAB64422 to AAB64470. AAB64471 to
 CC AAB64548 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Examples of activities include:
 CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
 CC cytostatic; cardiant; vasotropic; cerebroprotective; neutropic;
 CC neuroprotective; antibacterial; virucide; fungicide; and
 CC ophthalmological. The polynucleotides and polypeptides can be used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC culture, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities. AAF32690 to AAF32698 and
 CC AAB64421 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 1758 BP; 524 A; 380 C; 348 G; 504 T; 0 U; 2 Other;

Query Match 100.0%; Score 24; DB 4; Length 1758;
 Best Local Similarity 79.2%; Pred. No. 0.24;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCGCTCAGATAGGA 24
 Db 746 ATTCACACGAGGCGCTCAGATAGGA 769

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:50:11 ; Search time 2458.7 Seconds
(without alignments)
371.555 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 aauccaccagucgcauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	125	1	AI216602
2	24	100.0	127	1	BM725018
3	24	100.0	174	2	BE620536
C 4	24	100.0	176	7	T30356
C 5	24	100.0	179	5	BU963350
C 6	24	100.0	195	4	BG271724
C 7	24	100.0	196	7	F00105
C 8	24	100.0	207	7	Z38593
C 9	24	100.0	209	1	AA252742
C 10	24	100.0	237	1	AA989076
C 11	24	100.0	245	2	AW148462
12	24	100.0	247	1	AI796628
13	24	100.0	258	7	T82303
14	24	100.0	262	6	CD368992
C 15	24	100.0	267	2	BF734642
C 16	24	100.0	281	4	BG170953
17	24	100.0	287	7	F10097
18	24	100.0	287	7	F10120
19	24	100.0	287	7	T54784
20	24	100.0	289	7	T33248
21	24	100.0	290	1	AA176619
C 22	24	100.0	295	4	BG121948
C 23	24	100.0	301	1	AA906723
C 24	24	100.0	305	7	W46607

C 25	24	100.0	312	1	AA236753
26	24	100.0	321	2	AW468088
C 27	24	100.0	322	1	AI874377
C 28	24	100.0	341	1	AA236111
29	24	100.0	347	7	T34689
30	24	100.0	350	1	AI279315
31	24	100.0	351	5	BU681625
C 32	24	100.0	352	7	T31420
C 33	24	100.0	353	1	AV708414
C 34	24	100.0	354	4	BM452395
C 35	24	100.0	355	2	BE172028
36	24	100.0	365	1	AA084644
37	24	100.0	379	1	AA159037
C 38	24	100.0	382	1	AV682540
C 39	24	100.0	386	4	BM721543
40	24	100.0	386	7	N22319
C 41	24	100.0	390	1	AV648293
42	24	100.0	396	1	AI367513
C 43	24	100.0	396	1	AV648219
C 44	24	100.0	397	7	W37994
C 45	24	100.0	400	1	AA235659

ALIGNMENTS

RESULT 1
AI216602
LOCUS AI216602 125 bp mRNA linear EST 02-DEC-1998
DEFINITION qm33a05.xl NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1883600 3', mRNA sequence.
ACCESSION AI216602
VERSION AI216602.1 GI:3785643
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 965 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .125
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1883600"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu5"
/note="Organ: lung; Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Ronaldo."

ORIGIN

Matches	19; Conservative	5; Mismatches	0; Indels	0; Gaps	0
QY	1	AUCCACCAAGGCGCCAGAUAGGA	24		
Db	90	ATTCCACCAAGGCGCTCAGATAGGA	113		
RESULT 3					
LOCUS	BE620536	174 bp	mRNA	linear	EST 20-OCT-2000
DEFINITION	G01483007T1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885864	3',			
ACCESSION	BE620536				
VERSION	BE620536.1	GI:9891474			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 174)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs@mail.nih.gov				
	Tissue Procurement: DCTD/DTF/Gazdar				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				
	Plate: LLAM9661 row: m column: 01				
	High quality sequence start: 27				
	High quality sequence stop: 158.				
FEATURES	Location/Qualifiers				
source	1..174				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:3885864"				
	/tissue_type="large cell carcinoma, undifferentiated"				
	/lab_host="DH10B (phage-resistant)"				
	/clone_lib="NIH MGC 69"				
	/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."				
ORIGIN					
Query Match	100.0%;	Score 24;	DB 2;	Length 174;	
Best Local Similarity	79.2%;	Pred. No. 2;			
Matches	19; Conservative	5; Mismatches	0; Indels	0; Gaps	0; Gaps
QY	1	AUCCACCAAGGCGCCAGAUAGGA	24		
Db	24	ATTCCACCAAGGCGCTCAGATAGGA	47		
RESULT 4					
LOCUS	T30356/c	176 bp	mRNA	linear	EST 06-SEP-1995
DEFINITION	EST15349 Human Endothelial cells Homo sapiens cDNA 5' end similar to None, mRNA sequence.				
ACCESSION	T30356				
VERSION	T30356.1	GI:612454			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 176)				
	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,				

Bult, C.J., Lee, N., Kirkness, E.P., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, W.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinklejr, P.S., Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmatos, S.M., Merrick, J.M., Moreno-Palauques, R.P., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haezel, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)

JOURNAL
MEDLINE
PUBMED
COMMENT

Other ESTs: THC11414
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423

Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org)

Seq primer: M13 Reverse.

Location/Qualifiers

1. 176
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):100067"
/db_xref="taxon:9606"
/tissue_type="endothelial"
/clone_lib="Human Endothelial cells"

FEATURES
source

ORIGIN

Query Match 100.0%; Score 24; DB 7; Length 176;
Best Local Similarity 79.2%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGGUCUCAGAUAGGA 24
Db 101 ATTCCACGAGTGCCTCAGATAGGA 78

RESULT 5
BU963350/c
LOCUS BU963350 179 bp mRNA linear EST 21-OCT-2002
DEFINITION AGENCOURT 10616090 NIH MGC 141 Homo sapiens cDNA clone
IMAGE:6744396 5', mRNA sequence.

ACCESSION BU963350
VERSION BU963350.1 GI:24192922

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 179)
NIH-MGC <http://mgi.nci.nih.gov/>

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>

Plate: LFCM3085 row: j column: 11

High quality sequence stop: 179.

Location/Qualifiers

source

1. 179

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:6744396"

/tissue_type="mixed (pool of 40 RNAs)"

/lab_host="DH10B (Ti-phage-resistant)"

/clone_lib="NIH_MGC_141"

/note="vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);

Site_2: SfiI (ggcgctctggcc); Double-stranded cDNA was

prepared from a pool of 40 cell line polyA+ RNAs (bladder

- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -

4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,

kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,

ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary

gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were

used in cloning as follows:

5'-AAGCAGTGGTATCAACGAGTCGCGCATTCACGCGGG-3' and

5'-ATTCTAGAGCGCGGCGGCGACATG-dT(30)NN-3'. Full-length

enriched library was constructed using the Clontech

Creator SMART kit and size-selected to contain the 0.2-0.5

kb size fraction (other fractions present in NIH_MGC 142).

Library created in the laboratory of M. Brownstein (NIMH,

NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 24; DB 5; Length 179;

Best Local Similarity 79.2%; Pred. No. 2.2;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGGUCUCAGAUAGGA 24

Db 73 ATTCCACGAGTGCCTCAGATAGGA 50

RESULT 6

BU9271724

LOCUS

DEFINITION nai52907.x1 NCI_CGAP_HN20 Homo sapiens cDNA clone IMAGE:4263757 3',
mRNA sequence.

ACCESSION BU9271724

VERSION BU9271724.1 GI:12980154

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 195)

NCI/NIDR-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute / National Institute of Dental Research,

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL, send email to:

info@image.llnl.gov

Seq primer: -40UP from Gibco.

Location/Qualifiers

source

1. 195

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4263757"

/lab_host="DH10B"
 /clone_lib="NCI CGAP HN20"
 /note="Organ: normal head/neck tissue; Vector: pAMP1; mRNA
 made from head/neck tissue, cDNA made by oligo-dT
 priming. Directionally cloned into UDG sites.
 Size-selected on agarose gel, average insert size 300 bp.
 Primary library. cDNA Library Preparation: David B.
 Krizman, Ph.D."

ORIGIN

Query Match 100.0%; Score 24; DB 4; Length 195;
 Best Local Similarity 79.2%; Pred. No. 2.2;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAAGCCUACAGAUAGGA 24

Db 81 ATTCCACCAAGTCCTCAGATAGGA 104

RESULT 7
F00105/c

LOCUS F00105 196 bp mRNA linear EST 14-MAR-1995
 DEFINITION HSB21G041 STRATAGNE Human skeletal muscle cDNA library, cat.
 #936215. Homo sapiens cDNA clone 21G04, mRNA sequence.

ACCESSION F00105.1 GI:707366

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUFFRAY, C., BEHAR, G., BOIS, F., BOUCHIER, C., DA SILVA, C.,
 DEVIGNES, M.D., DUPRAT, S., HOULGATTE, R., JUMEAU, M.N., LAMY, B.,
 LORENZO, F., MITCHELL, H., MARIAGE-SAMSON, R., PIETU, G., POULIOT, Y.,
 SEBASTIANI-KABAKTCHIS, C. and TESSIER, A.
 IMAGE: molecular integration of the analysis of the human genome
 and its expression

TITLE

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

JOURNAL 95277534

MEDLINE 7757816

PUBMED

COMMENT

Contact: Genethon
 Genexpress-Genethon
 Genethon Centre de recherche sur le Genome Humain
 1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE

Tel: 33169472800

Fax: 33160778698

Email: genexpress@genethon.fr

Single read.

Seq primer: (-21)M13 universal.

Location/Qualifiers

1..196

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="21G04"

/sex="Female"

/tissue_type="skeletal muscle"

/dev_stage="19 years"

/clone_lib="STRATAGNE Human skeletal muscle cDNA library,

cat. #936215."

/notes="Organ: leg muscle; Vector: Lambda ZAPII; Tissue

from female, 19 years old, normal leg muscle. Cloning

vector is Lambda ZAPII, in vivo excision from lambda ZAPII

to pBluescript SK(+). Genexpress library reference is B."

ORIGIN

Query Match 100.0%; Score 24; DB 7; Length 196;
 Best Local Similarity 79.2%; Pred. No. 2.2;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAAGCCUACAGAUAGGA 24

Db 81 ATTCCACCAAGTCCTCAGATAGGA 104

Db 77 ATTCCACCAAGTCCTCAGATAGGA 54

RESULT 8

Z38593

LOCUS

DEFINITION

Z38593

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT

Genethon

Genexpress-Genethon

Genethon Centre de recherche sur le Genome Humain

1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE

Tel: 33169472800

Fax: 33160778698

Email: genexpress@genethon.fr

Single read.

Seq primer: (-21)M13 universal.

Location/Qualifiers

1..207

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="c-0hb08"

/sex="Female"

/tissue_type="total brain"

/dev_stage="3 months old"

/clone_lib="normalized infant brain cDNA"

/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;

Site 2: NotI; sex:Female; dev_stage=3 months old;

isolate=muscular atrophy patient; tissue_type=total

brain; total mRNA was oligo-(dT) primed and directionally

cloned 5' -> 3' into the HindIII -> NotI sites of the

lafmid BA vector. Clone library from B.Soaes, Psychiatry

Dept. Columbia University, USA

Normalization_method:

Bento Soares, P.N.A.S in press"

ORIGIN

Query Match 100.0%; Score 24; DB 7; Length 207;

Best Local Similarity 79.2%; Pred. No. 2.2;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAAGCCUACAGAUAGGA 24

Db 76 ATTCCACCAAGTCCTCAGATAGGA 99

RESULT 9
AA252742/c

LOCUS

DEFINITION

AA252742

ACCESSION

VERSION

KEYWORDS

SOURCE

AA252742 209 bp mRNA linear EST 13-AUG-1997
 zs26a12.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686302 5',
 mRNA sequence.

AA252742

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 209)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 210
Insert Length: 738 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES
source
1..209
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5590445"
/db_xref="taxon:9606"
/clone="IMAGE:686302"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCBI"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTACCAATCTGAAGTGGAGCGCGCGCTCAATTTTTTTTTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 100.0%; Score 24; DB 1; Length 209;
Best Local Similarity 79.2%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCUCCAGAUAGGA 24
|:|||||:|||||:|||||:|||||
Db 136 ATTCACCAAGTGCCTCAGATAGGA 113

RESULT 10
AA989076/c
LOCUS AA989076
DEFINITION or88e02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602938 3',
mRNA sequence.
ACCESSION AA989076
VERSION AA989076.1 GI:3174647
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 237)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 210
Insert Length: 738 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES
source
1..237
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1602938"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 100.0%; Score 24; DB 1; Length 237;
Best Local Similarity 79.2%; Pred. No. 2.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCUCCAGAUAGGA 24
|:|||||:|||||:|||||:|||||
Db 127 ATTCACCAAGTGCCTCAGATAGGA 104

RESULT 11
AA148462
LOCUS AA148462
DEFINITION xfl4e04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618046 3',
mRNA sequence.
ACCESSION AA148462
VERSION AA148462.1 GI:6196358
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 245)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 241.

FEATURES
source
1..245
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2618046"
/tissue_type="renal cell tumor"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid8"

```

/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.2 kb. Life Technologies catalog #:
11524-014"

ORIGIN

```

Query Match      100.0%; Score 24; DB 2; Length 245;
Best Local Similarity 79.2%; Pred.No. 2.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUCAGAUAGGA 24
Db 77 ATTCCACAGTGCTCAGATAGGA 100

```

RESULT	12
AJ796628	
LOCUS	AI796628 linear EST 20-DEC-1999
DEFINITION	wH58G01.x1 NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2384976 ', mRNA sequence.
ACCESSION	AI796628
VERSION	AI796628.1 GI:5362091
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1. (bases 1 to 247)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

```

FEATURES
source
seq primer: -400f from GiBCCO.
Location/Qualifiers
1. 247
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2384976"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneId3 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Patima Bonaldo."

```

```

ORIGIN
Query Match      100.0%; Score 24; DB 1; Length 247;
Best Local Similarity 79.2; Pred.No. 2.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCGAGUGCCUCAGAUAGGA 24
      : : : : : : : : : : : : : :
Db 81 ATTCCACGAGTGCCTCAGATAGGA 104

```

RESULT 13	FEATURES
T82303	SOURCE
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES .
source

ORIGIN

```

Query Match      100.0%; Score 24; DB 7; Length 258;
Best Local Similarity 79.2%; Pred.No. 2.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCCAGUGCCUCAGAUAGGA 24
Db 90 ATTCCACCCAGTGCTCAGATAGGA 113

```

RESULT 14
 CD368992
 LOCUS
 DEFINITION
 UI-H-FT1-bjx-f-24-0-UI.s1 NCI_CGAP_FTI Homo sapiens cDNA clone
 UI-H-FT1-bjx-f-24-0-UI 3', mRNA sequence.
 CD368992
 ACCESSION
 VERSION
 CD368992.1 GI:31153082
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 262)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE
 Tumor Gene Index
 COMMENT
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.

FEATURES

Location/Qualifiers

source

```

1. .262
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ftl-bjx-f-24-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="PH108 (Life Technologies)"
/clone_lib="NCI_CGAP_FTL"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FTL is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP) moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP) moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT73-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCGG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG LIB=UI-H-Ftl
TAG_SEQ=GGCCATGCGG

```

ORIGIN

```

Query Match      100.0%; Score 24; DB 6; Length 262;
Best Local Similarity 79.2%; Pred. No. 2.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUCAGAUAGGA 24
   |:|||||:|||||:|||||:|||||
DB 92 ATTCCACCAGTGCCTCAGATAGGA 115

```

RESULT 15

```

BF734642/c
LOCUS
DEFINITION
ACCESSION   BF734642
VERSION
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 267)
AUTHORS
Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

```

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

```

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC6&t2=RC6-AN0068-
301100-012-B11&t3=2000-11-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 244.

```

FEATURES

source

```

1. .267
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0068"
/note="Organ: amnion normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

ORIGIN

```

Query Match      100.0%; Score 24; DB 2; Length 267;
Best Local Similarity 79.2%; Pred. No. 2.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUCAGAUAGGA 24
   |:|||||:|||||:|||||:|||||
DB 141 ATTCCACCAGTGCCTCAGATAGGA 118

```

```

Search completed: July 30, 2005, 15:01:03
Job time : 2461.7 secs

```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:52:26 ; Search time 86.5946 Seconds
(without alignments)
453.500 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 auuccaccagucccagauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCUTUS_COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	496	4	US-09-513-999C-11204
C 2	24	100.0	4822	3	US-09-484-970B-106
C 3	22	91.7	211	3	US-09-506-729-51
C 4	22	91.7	1669	4	US-09-949-016-3253
C 5	22	91.7	2610	4	US-09-023-655-382
C 6	22	91.7	42075	4	US-09-949-016-14995
C 7	18.8	78.3	601	4	US-09-949-016-31983
C 8	18.8	78.3	601	4	US-09-949-016-70441
C 9	18.8	78.3	246230	4	US-09-949-016-17019
C 10	18.8	78.3	246230	4	US-09-949-016-17020
C 11	18.8	78.3	246230	4	US-09-949-016-17021
C 12	18.8	78.3	246230	4	US-09-949-016-17022
C 13	18.4	76.7	321022	4	US-09-949-016-11852
C 14	18.4	76.7	321022	4	US-09-949-016-14166
C 15	18.2	75.8	64593	4	US-09-949-016-16654
C 16	18.2	75.8	64593	4	US-09-949-016-16655
C 17	18.2	75.8	64593	4	US-09-949-016-16656
C 18	18.2	75.8	99498	4	US-09-949-016-12621
C 19	18.2	75.8	146428	4	US-09-949-016-12620
C 20	18.2	75.8	146438	4	US-09-949-016-12081
C 21	17.6	73.3	601	4	US-09-949-016-31982
C 22	17.6	73.3	601	4	US-09-949-016-31984
C 23	17.6	73.3	601	4	US-09-949-016-62026
C 24	17.6	73.3	601	4	US-09-949-016-70440
C 25	17.6	73.3	601	4	US-09-949-016-70442
C 26	17.6	73.3	1001	3	US-09-641-638-201
C 27	17.6	73.3	1001	3	US-09-641-638-202

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C 28 17.6 73.3 1001 4 US-10-170-097-201 Sequence 201, App
C 29 17.6 73.3 1001 4 US-10-170-097-202 Sequence 202, App
C 30 17.6 73.3 60002 4 US-09-949-016-12464 Sequence 12464, A
C 31 17.6 73.3 60003 4 US-09-949-016-13823 Sequence 13823, A
C 32 17.6 73.3 314798 4 US-09-949-016-13539 Sequence 13539, A
C 33 17.2 71.7 601 4 US-09-949-016-146829 Sequence 146829, A
C 34 17.2 71.7 601 4 US-09-949-016-146830 Sequence 146830, A
C 35 17.2 71.7 601 4 US-09-949-016-146831 Sequence 146831, A
C 36 17.2 71.7 601 4 US-09-949-016-146832 Sequence 146832, A
C 37 17.2 71.7 96340 4 US-09-949-016-15863 Sequence 15863, A
C 38 16.8 70.0 3456 4 US-09-023-905A-5 Sequence 5, Appli
C 39 16.8 70.0 4382 4 US-09-023-905A-3 Sequence 3, Appli
C 40 16.8 70.0 103377 4 US-09-949-016-14089 Sequence 14089, A
C 41 16.6 69.2 588 3 US-09-221-298-75 Sequence 75, Appl
C 42 16.6 69.2 588 4 US-09-401-064-75 Sequence 75, Appl
C 43 16.6 69.2 675 1 US-08-707-793A-3 Sequence 3, Appli
C 44 16.6 69.2 675 1 US-08-707-792A-3 Sequence 3, Appli
C 45 16.6 69.2 2129 4 US-09-016-434-1452 Sequence 1452, Ap

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ALIGNMENTS

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RESULT 1
US-09-513-999C-11204/c
; Sequence 11204, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11204
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 486
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-11204

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Query Match 100.0%; Score 24; DB 4; Length 496;

Best Local Similarity 79.2%; Pred. No. 0.033; Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AUUCCACCGUCCUCCAGAUAGGA 24
DB 410 ATTCCACCGAGTCCCTCAGATAGGA 387

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RESULT 2

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US-09-484-970B-106/c
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program

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; SEQ ID NO 106
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match 100.0%; Score 24; DB 3; Length 4822;
Best Local Similarity 79.2%; Pred. No. 0.05; Indels 0; Gaps 0;
Matches 19; Conservative 5; Mismatches 0

QY 1 AUUCCACCAGGCGCCUCAGAUAGGA 24
|:|||||:|||||:
Db 4099 ATCCACCAGTGCCTCAGATAGGA 4076

RESULT 3
US-09-506-729-51/c
; Sequence 51, Application US/09506729
; Patent No. 6365352
; GENERAL INFORMATION:
; APPLICANT: Yerramilli, Subrahmanyam V.
; APPLICANT: Praahar, Yatindra
; APPLICANT: Newberger, Peter
; APPLICANT: Goguen, Jon
; APPLICANT: Weisman, Sherman M.
; TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
; FILE REFERENCE: 44921-5016-US
; CURRENT APPLICATION NUMBER: US/09/506.729
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: PCT/US98/17284
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 60/056,844
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 51
; LENGTH: 211
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-506-729-51

Query Match 91.7%; Score 22; DB 3; Length 211;
Best Local Similarity 77.3%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 17; Conservative 5; Mismatches 0

QY 1 AUUCCACCAGGCGCCUCAGAUAG 22
|:|||||:|||||:
Db 148 ATCCACCAGTGCCTCAGATAG 127

RESULT 4
US-09-949-016-3253/c
; Sequence 3253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3253
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253

Query Match 91.7%; Score 22; DB 4; Length 1669;
Best Local Similarity 77.3%; Pred. No. 0.4; Indels 0; Gaps 0;
Matches 17; Conservative 5; Mismatches 0

QY 1 AUUCCACCAGGCGCCUCAGAUAG 22
|:|||||:|||||:
Db 1083 ATCCACCAGTGCCTCAGATAG 1062

RESULT 5
US-09-023-655-382/c
; Sequence 382, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT14
; CLONE: 1508778
US-09-023-655-382

Query Match 91.7%; Score 22; DB 4; Length 2610;
Best Local Similarity 77.3%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 17; Conservative 5; Mismatches 0

QY 1 AUUCCACCAGGCGCCUCAGAUAG 22
|:|||||:|||||:

Db 2148 ATCCACCAGTGCCTCAGATAG 2127

RESULT 6

US-09-949-016-14995/c
; Sequence 14995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14995
; LENGTH: 42075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14995

Query Match 91.7%; Score 22; DB 4; Length 42075;
Best Local Similarity 77.3%; Pred. No. 0.72;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGGCGCUCAGAUAG 22

Db 39488 ATCCACCAGTGCCTCAGATAG 39467

RESULT 7

US-09-949-016-31983/c
; Sequence 31983, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31983
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-31983

Query Match 78.3%; Score 18.8; DB 4; Length 601;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AUUCCACCAGGCGCUCAGAUAGGA 24

Db 307 ATTCAYGAGTGCCACAGTTAGGA 284

RESULT 8

US-09-949-016-70441/c

; Sequence 70441, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70441
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-70441

Query Match 78.3%; Score 18.8; DB 4; Length 601;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AUUCCACCAGGCGCUCAGAUAGGA 24

Db 307 ATTCAYGAGTGCCACAGTTAGGA 284

RESULT 9

US-09-949-016-17019/c
; Sequence 17019, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17019
; LENGTH: 246230
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(246230)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17019

Query Match 78.3%; Score 18.8; DB 4; Length 246230;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 UUCCACCAGGCGCUCAGAUAGG 23

Db 134516 TTCCACCAGTGCCTCAACAGG 134495

RESULT 10

US-09-949-016-17020/c
; Sequence 17020, Application US/09949016

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17020
; LENGTH: 246230
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(246230)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17020

Query Match      78.3%; Score 18.8; DB 4; Length 246230;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 UUCCACCAGUGCCUCAGAUAGG 23
Db      134516 TTCCACCAGTGCCTCAACAGG 134495

RESULT 11
US-09-949-016-17021/c
; Sequence 17021, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17021
; LENGTH: 246230
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(246230)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17021

Query Match      78.3%; Score 18.8; DB 4; Length 246230;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 UUCCACCAGUGCCUCAGAUAGG 23
Db      134516 TTCCACCAGTGCCTCAACAGG 134495
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RESULT 12
US-09-949-016-17022/c
; Sequence 17022, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17022
; LENGTH: 246230
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(246230)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17022

Query Match      78.3%; Score 18.8; DB 4; Length 246230;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 UUCCACCAGUGCCUCAGAUAGG 23
Db      134516 TTCCACCAGTGCCTCAACAGG 134495

RESULT 13
US-09-949-016-11852/c
; Sequence 11852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11852
; LENGTH: 321022
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(321022)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11852

Query Match      76.7%; Score 18.4; DB 4; Length 321022;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      3 UCCACCAGUGCCUCAGAUAG 22
          :|||||:|||||:|||||
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Db 287950 TCACACAGTGCCTCAGAGAG 287931

RESULT 14

US-09-949-016-14166/c
; Sequence 14166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14166
; LENGTH: 321022
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(321022)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14166

Query Match 76.7%; Score 18.4; DB 4; Length 321022;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 UCCACAGUGCCUCAGAUAG 22

Db 287950 TCACACAGTGCCTCAGAGAG 287931

RESULT 15

US-09-949-016-16654/c
; Sequence 16654, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16654
; LENGTH: 64593
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(64593)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16654

Query Match 75.8%; Score 18.2; DB 4; Length 64593;
Best Local Similarity 65.2%; Pred. No. 59;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 UUCACACAGUGCCUCAGAUAGGA 24
Db 55591 TTCCACACAGTGTCTCAGGTAGCA 55569

Search completed: July 30, 2005, 15:05:46
Job time : 89.5946 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
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C 2	17	68.0	17	6	AX215987	Sequence
C 3	17	68.0	17	6	AX215988	Sequence
C 4	17	68.0	17	6	AX216295	Sequence
C 5	17	68.0	17	6	AX216587	Sequence
C 6	17	68.0	17	6	AX216842	Sequence
C 7	16.4	65.6	22	6	AX481558	Sequence
C 8	16.4	65.6	24	6	AX481559	Sequence
C 9	16	64.0	17	6	AX216586	Sequence
C 10	15.8	63.2	60	6	CQ535926	Sequence
C 11	15.4	61.6	20	6	AR225975	Sequence
C 12	15.4	61.6	51	6	AX160170	Sequence
C 13	15	60.0	17	6	AX215989	Sequence
C 14	15	60.0	60	6	CQ537946	Sequence
C 15	15	60.0	60	6	CQ550775	Sequence
C 16	14.6	58.4	24	6	CQ816744	Sequence
C 17	14.4	57.6	17	6	AR401760	Sequence
C 18	14.4	57.6	17	6	AX722986	Sequence
C 19	14.4	57.6	17	6	BD067260	Enzymatic

ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1429 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
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Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAUAGCUUGGAUCACAC 20
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Db 17 GATAGCTTGGATCACAC 1
RESULT 3
AX215988/c 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 1430 from Patent WO0159103.
ACCESSION AX215988
VERSION AX215988.1 GI:15526031
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1430 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 3 GGAUAGCUUGGAUCACA 19
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RESULT 4
AX216295/c 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 1737 from Patent WO0159103.
ACCESSION AX216295
VERSION AX216295.1 GI:15526356
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression
Patent: WO 0159103-A 1737 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 8 GCUUGAUCACACCCUU 24
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Db 17 GCTTGGATCACACCCCTT 1
RESULT 5
AX216587/c 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 2029 from Patent WO0159103.
ACCESSION AX216587
VERSION AX216587.1 GI:15526648
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2029 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
AX216842/c 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 2284 from Patent WO0159103.
ACCESSION AX216842
VERSION AX216842.1 GI:15526903
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2284 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers

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ORIGIN

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Db 17 AGCTGGATCACCCCT 1

RESULT 7
AX481558/c
LOCUS
DEFINITION
Sequence 172 from Patent WO02055693.
ACCESSION
AX481558
VERSION
AX481558.1 GI:22316472
KEYWORDS
synthetic construct
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
TITLE
Method for inhibiting the expression of a target gene
JOURNAL
Patent: WO 02055693-A 172 18-JUL-2002;
Ribopharma AG (DE)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="sense-Strang (ES-2A) einer dsRNA, die homolog zur
humanen EGFR-Sequenz ist"

ORIGIN

Query Match
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Db 19 GGACAGCTTGGATCACAC 2

RESULT 8
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LOCUS
DEFINITION
Sequence 173 from Patent WO02055693.
ACCESSION
AX481559
VERSION
AX481559.1 GI:22316473
KEYWORDS
synthetic construct
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
TITLE
Method for inhibiting the expression of a target gene
JOURNAL
Patent: WO 02055693-A 173 18-JUL-2002;
Ribopharma AG (DE)
FEATURES
source
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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ORIGIN
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Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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RESULT 9
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LOCUS
DEFINITION
Sequence 2028 from Patent WO0159103.
ACCESSION
AX216586
VERSION
AX216586.1 GI:15526647
KEYWORDS
synthetic construct
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 2028 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

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Best Local Similarity 64.0%; Score 16; DB 6; Length 17;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 17 TTGGATCACACCCCTTG 2

RESULT 10
CQ535926/c
LOCUS
DEFINITION
Sequence 5561 from Patent WO0210449.
ACCESSION
CQ535926
VERSION
CQ535926.1 GI:41502190
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL
Patent: WO 0210449-A 5561 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source
1. .60
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

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LOCUS	AR225975 20 bp DNA linear PAT 20-DEC-2002
DEFINITION	Sequence 38 from patent US 6444465.
ACCESSION	AR225975
VERSION	AR225975.1 GI:27264129
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 20)
AUTHORS	Wyatt, J. and Freier, S.M.
TITLE	Antisense modulation of Her-1 expression
JOURNAL	Patent: US 6444465-A 38 03-SEP-2002;
FEATURES	Location/Qualifiers source 1..20 /organism="unknown" /mol_type="genomic DNA"
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Db	4 GGACAGCTTGGATCACA 20 ::: :
RESULT 12	
LOCUS	AX160170/c 51 bp DNA linear PAT 22-JUN-2001
DEFINITION	Sequence 3498 from Patent WO0140521.
ACCESSION	AX160170
VERSION	AX160170.1 GI:14541501
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Shimkets, R.A. and Leach, M.
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL	Patent: WO 0140521-A 3498 07-JUN-2001;
FEATURES	Curagen Corporation (US) Location/Qualifiers source 1..51 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
misc_feature	26 /note="#2 of 2 allelic variants (3497 is other entry)" Accession number CG43284565"
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LOCUS	AX215989/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION	Sequence 1431 from Patent WO0159103.
ACCESSION	AX215989
VERSION	AX215989
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL	Patent: WO 0159103-A 1431 16-AUG-2001;
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US) Location/Qualifiers source 1..17 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Nucleic Acid"
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Best Local Similarity	66.7%; Pred. No. 1.7e+04;
Matches	10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14	
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DEFINITION	Sequence 7581 from Patent WO0210449.
ACCESSION	CQ537946
VERSION	CQ537946.1 GI:41504210
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE	Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL	Patent: WO 0210449-A 7581 07-FEB-2002;
FEATURES	Compugen Inc. (US) Location/Qualifiers source 1..60 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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DEFINITION	Sequence 20410 from Patent WO0210449.
ACCESSION	CQ550775
VERSION	CQ550775.1 GI:41517202
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL	Patent: WO 0159103-A 1431 16-AUG-2001;
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US) Location/Qualifiers source 1..17 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Nucleic Acid"
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Matches	10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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Db	15 CTGGATAGCTTGAT 1 ::: :

REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 20410 07-FEB-2002;
Compugen Inc. (US)
FEATURES Location/Qualifiers
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Matches 13; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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Db 25 TGGAAAGTTTGGAAACACATACCTT 3

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:18:17 ; Search time 307.77 Seconds
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Title: US-09-544-776-3
Perfect score: 25
Sequence: 1 cuggauagcuggaucacacccuug 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 4316768

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	17	68.0	17	4 ABK00561	ABK00561 Human NOG
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4	17	68.0	17	4 ABK01430	ABK01430 Human NOG
5	17	68.0	17	4 ABK02029	ABK02029 Human NOG
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9	16.6	66.4	58	10 ACD28188	Acad28188 Human rep
10	16.4	65.6	22	6 ABV78288	Abv78288 Human EGF
11	16.4	65.6	24	6 ABV78289	Abv78289 Human EGF
12	16.2	64.8	25	12 ADH72558	Adh72558 Human pro
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14	15.8	63.2	60	6 ABN32813	Abn32813 Human spl
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18	15	60.0	17	4 ABK01431	ABK01431 Human NOG
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20	15	60.0	60	6 ABN34833	Abn34833 Human spl

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C 23	14.4	57.6	17	2	AAV97320	Aav97320 Human EGF
C 24	14.4	57.6	17	8	ACC63426	Acc63426 Murine ol
25	14.4	57.6	20	12	ADJ17724	Adj17724 Antisense
26	14.4	57.6	20	12	ADJ17550	Adj17550 Antisense
27	14.4	57.6	20	12	ADJ17838	Adj17838 Antisense
28	14.4	57.6	20	12	ADJ16551	Adj16551 Antisense
29	14.4	57.6	20	12	ADJ17868	Adj17868 Antisense
C 30	14.4	57.6	25	10	ADC05670	Adc05670 Human Na/
C 31	14.4	57.6	25	10	ADC05669	Adc05669 Human Na/
C 32	14.4	57.6	60	6	ABN33385	Abn33385 Human spl
C 33	14.4	57.6	60	6	ABN42423	Abn42423 Human spl
34	14.2	56.8	24	6	ABL53901	AbL53901 Human rib
35	14.2	56.8	25	9	ACK21293	Ack21293 Human mic
36	14.2	56.8	28	4	AAH91639	Aah91639 Human inf
37	14.2	56.8	31	2	AAQ37571	Aaq37571 HCV conse
38	14.2	56.8	31	2	AAT64885	Aat64885 Hepatitis
C 39	14.2	56.8	37	4	AAH91211	Aah91211 Human inf
C 40	14.2	56.8	51	4	AAI79791	Aai79791 Human non
41	14.2	56.8	60	6	ABN50365	Abn50365 Human spl
42	14.2	56.8	60	6	ABN37067	Abn37067 Human spl
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C 44	14	56.0	17	4	ABK02027	Abk02027 Human NOG
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ALIGNMENTS

RESULT 1
AAC64407
ID AAC64407 standard; RNA; 25 BP.
XX AAC64407;

DT 08-FEB-2001 (first entry)
XX

DE Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:3.
XX Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
KW stress-phosphorylated endoplasmic reticulum protein; cytosolic;
KW gene therapy; cell growth; cellular stress response; neuron growth;
KW regulator of oxidative stress; inhibitor of neurite outgrowth;
KW axon regeneration; diagnosis; cancer; identification; antisense;
KW phosphorothioate; ss.
XX Homo sapiens.
XX

Key Location/Qualifiers
FH modified_base 1..25
FT /*tag= a
FT /note= "phosphorothioate linkages"

XX WO2000060083-A1.

PN 12-OCT-2000.

PD 07-APR-2000; 2000WO-US009383.

PR 08-APR-1999; 99US-0128372P.

PR 21-JUN-1999; 99US-0140331P.

PA (CHIR) CHIRON CORP.

PI Wei D, Halenbeck R, Williams LT;

XX WPI; 2000-665007/64.

XX Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic
 CC reticulum protein, designated Nogo B. Nogo B has cytostatic activity and
 CC is a modulator of the storage and exchange of calcium, cell growth and
 CC cellular stress response. It can: regulate oxidative stress; inhibit
 CC neurite outgrowth, neuron growth and axon regeneration. Nogo B
 CC polypeptides and polynucleotides are useful for modulating stress levels
 CC and cellular stress-response, cell growth and viability, diagnosis and
 CC treatment of cancer, malignant growth and other Nogo B related diseases.
 CC Nogo B polypeptides are also useful to screen combinatorial libraries to
 CC identify agonist or antagonist. Antibodies against Nogo B polypeptides
 CC are useful for affinity chromatography and distinguishing Nogo B
 CC polypeptides. The present sequence represents a human Nogo B
 CC phosphorothioate antisense oligonucleotide from the present invention

SQ Sequence 25 BP; 5 A; 7 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUACCUUGGAUCACACCCUUG 25
 |||||
 Db 1 CUGGAUACCUUGGAUCACACCCUUG 25

RESULT 2

ABK0561/c
 ID ABK00561 standard; RNA; 17 BP.
 AC ABK00561;
 DT 12-MAR-2002 (first entry)
 XX Human Nogo Hammerhead Ribozyme #561.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Creutzfeldt-Jakob disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004273.
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 XX central nervous system injury.
 XX Claim 88; Page 74; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (Nogo). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The Nogo-
 CC targeting nucleic acid is used to cleave RNA of the Nogo gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce Nogo activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC Nogo. The treatment may further comprise the use of one or more
 CC therapies. In particular, the Nogo-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of Nogo expression. The present
 CC sequence is a hammerhead ribozyme of the invention

SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 68.0%; Score 17; DB 4; Length 17;
 Best Local Similarity 76.5%; Pred. No. 3.3e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AUAAGCUUGGAUCACACC 21
 |||||
 Db 17 ATAGCTTGGATCACACC 1

RESULT 3

ABK01737/c
 ID ABK01737 standard; RNA; 17 BP.
 XX ABK01737;
 XX 12-MAR-2002 (first entry)
 XX Human Nogo Zinzyme #59.
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX Homo sapiens.

OS Synthetic.
 XX WO200159103-A2.
 FN
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 DR
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 88; Page 95; 200pp; English.
 FS
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a NYN motif) or
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zinzyme molecule of the invention
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;
 Query Match 68.0%; Score 17; DB 4; Length 17;
 Best Local Similarity 70.6%; Pred. No. 3.3e+02;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Oy 8 GCUGGGAUCACACCCUU 24
 ||:|||||:
 Db 17 GCTTGGATCACACCCCT 1
 ||:|||||:
 RESULT 4
 ABK01430/c

ID ABK01430 standard; RNA; 17 BP.
 XX AC
 XX ABK01430;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 XX Human NOGO Inozyme #700.
 DE
 XX
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX
 PN WO200159103-A2.
 XX
 XX 16-AUG-2001.
 PD
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 PF
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 XX
 XX 28-FEB-2000; 2000US-0185516P.
 PR
 XX 06-MAR-2000; 2000US-0187128P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 DR
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 PT
 XX
 XX Claim 88; Page 89; 200pp; English.
 PS
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a NYN motif) or
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zinzyme molecule of the invention
 XX

therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an inozyme of the invention

Sequence 17 BP; 4 A; 5 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 68.0%; Score 17; DB 4; Length 17;
Best Local Similarity 76.5%; Pred. No. 3.3e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGAUAGCUUGGAUACA 19
Db 17 GGATAGCTTGGATCA 1

RESULT 5
ID ABRK02029 standard; RNA; 17 BP.
XX
AC ABRK02029;
DT 12-MAR-2002 (first entry)
DE Human NOGO Zinzyme #351.
XX
Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.
OS Synthetic.
XX WO200159103-A2.
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX 28-FEB-2000; 2000US-0185516P.
XX 06-MAR-2000; 2000US-0187128P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
XX
XX Claim 88; Page 101; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates

expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNazyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is a zinzyme molecule of the invention

Sequence 17 BP; 5 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 68.0%; Score 17; DB 4; Length 17;
Best Local Similarity 70.6%; Pred. No. 3.3e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCA 17
Db 17 CTGGATAGCTTGGATCA 1

RESULT 6
ABK01429/c
ID ABRK01429 standard; RNA; 17 BP.
XX
AC ABRK01429;
XX
DT 12-MAR-2002 (first entry)
DE Human NOGO Inozyme #699.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.
OS Synthetic.
XX WO200159103-A2.
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 89; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 68.0%; Score 17; DB 4; Length 17;
 Best Local Similarity 76.5%; Pred. No. 3.3e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 GAUAGCUUGGAUCACAC 20
 ||:||||:|||||
 Db 17 GATAGCTTGGATCACAC 1
 RESULT 7
 ABK02284/c
 ID ABK02284 standard; RNA; 17 BP.
 XX
 AC ABK02284;
 XX
 DT 12-MAR-2002 (first entry)
 XX Human NOGO DNzyme #196.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PF 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 115; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention

```
CC sequence is a DNazyme molecule of the invention
XX Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;
SQ
    Query Match      68.0%; Score 17; DB 4; Length 17;
    Best Local Similarity 76.5%; Pred. No. 3.3e+02;
    Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCUUGGAUCACACCCU 23
Db 17 AGCTTGGATCACACCT 1

RESULT 8
ADF73036/c
ID ADF73036 standard; cDNA; 58 BP.
XX
AC ADF73036;
XX
DT 12-FEB-2004 (first entry)
XX
DE DNA sequence of the invention #6.
XX
KW human repair gene DNA polymerase beta; gene therapy; esophagus cancer;
KW ss.
OS Synthetic.
XX
XX CN1366047-A.
PN
PD 28-AUG-2002.
XX
PF 24-AUG-2001; 2001CN-00128374.
XX
PR 24-AUG-2001; 2001CN-00128374.
XX
PA (UYZH-) UNIV ZHENGZHOU.
XX
PI Dong Z, Zhao G, Zhao Q;
XX
WPI; 2003-240398/24.
XX
Human DNA polymerase beta mutant gene and its corresponding protein.
Claim 3; Page 2; 11pp; Chinese.
XX
CC The present invention discloses a cDNA sequence of human repair gene DNA
CC polymerase beta, which is a specific representation of DNA polymerase
CC beta in esophagus cancer. The protein coded by it has fully lost the DNA
CC repair activity of DNA polymerase beta. It can be used for early
CC diagnosis and gene therapy of esophagus cancer. This sequence represents
CC a human DNA polymerase beta associated oligonucleotide
XX
SQ Sequence 58 BP; 22 A; 14 C; 11 G; 11 T; 0 U; 0 Other;
    Query Match      66.4%; Score 16.6; DB 10; Length 58;
    Best Local Similarity 52.2%; Pred. No. 6.1e+02;
    Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 UGGAUAGCUUGAUCACACCCUU 24
Db 38 TGGATAGCTTGGCTCACGTTCTT 16

RESULT 10
ABV78288/c
ID ABV78288 standard; RNA; 22 BP.
XX
AC ABV78288;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human EGFR inhibitor dsRNA sense strand SEQ ID NO 172.
XX
KW RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoacide; ds.
XX
OS Homo sapiens.
XX
PN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
WPI; 2002-590671/63.
DE
```

```
XX
KW Human; repair gene; DNA polymerase beta; oesophagus cancer;
KW DNA repair activity; gene therapy; ss.
XX
OS Unidentified.
XX
PN CN1366047-A.
XX
PD 28-AUG-2002.
XX
PF 24-AUG-2001; 2001CN-00128374.
XX
PR 24-AUG-2001; 2001CN-00128374.
XX
PA (UYZH-) UNIV ZHENGZHOU.
XX
PI Dong Z, Zhao G, Zhao Q;
XX
WPI; 2003-240398/24.
XX
Human DNA polymerase beta mutant gene and its corresponding protein.
Claim 3; Page 2; 11pp; Chinese.
XX
CC The present invention discloses a cDNA sequence of human repair gene DNA
CC polymerase beta, which is a specific representation of DNA polymerase
CC beta in esophagus cancer. The protein coded by it has fully lost the DNA
CC repair activity of DNA polymerase beta. It can be used for early
CC diagnosis and gene therapy of esophagus cancer. This sequence represents
CC a human DNA polymerase beta associated oligonucleotide
XX
SQ Sequence 58 BP; 22 A; 14 C; 11 G; 11 T; 0 U; 0 Other;
    Query Match      66.4%; Score 16.6; DB 10; Length 58;
    Best Local Similarity 52.2%; Pred. No. 6.1e+02;
    Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 UGGAUAGCUUGAUCACACCCUU 24
Db 38 TGGATAGCTTGGCTCACGTTCTT 16

RESULT 10
ABV78288/c
ID ABV78288 standard; RNA; 22 BP.
XX
AC ABV78288;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human EGFR inhibitor dsRNA sense strand SEQ ID NO 172.
XX
KW RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoacide; ds.
XX
OS Homo sapiens.
XX
PN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
WPI; 2002-590671/63.
DE
```


XX Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
XX target and having an overhang.
XX
XX Claim 13; Page 40; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a dsRNA molecule related to the invention
XX
XX Sequence 22 BP; 6 A; 6 C; 5 G; 0 T; 5 U; 0 Other;
SQ
Query Match 65.6%; Score 16.4; DB 6; Length 22;
Best Local Similarity 77.8%; Pred. No. 6.6e+02;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAAUAGCTUGGAUCACAC 20
Db 19 GGACAGCTTGGATCACAC 2

RESULT 11
ABV78289
ID ABV78289 standard; RNA; 24 BP.
XX
AC ABV78289;
XX
XX 15-NOV-2002 (first entry)
XX
XX Human EGFR inhibitor dsRNA antisense strand SEQ ID NO 173.
XX
XX RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
XX virucide; protozoacide; ds.
XX
XX Homo sapiens.
XX
XX WO200255693-A2.
XX
XX 18-JUL-2002.
XX
XX 09-JAN-2002; 2002WO-EP000152.
XX
XX 09-JAN-2001; 2001DE-01000586.
XX 26-OCT-2001; 2001DE-01055280.
XX 29-NOV-2001; 2001DE-01058411.
XX 07-DEC-2001; 2001DE-01060151.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
XX
XX Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
XX Claim 13; Page 40; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1

CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a dsRNA molecule related to the invention
XX
XX Sequence 24 BP; 5 A; 5 C; 6 G; 0 T; 8 U; 0 Other;
SQ
Query Match 65.6%; Score 16.4; DB 6; Length 24;
Best Local Similarity 94.4%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAAUAGCTUGGAUCACAC 20
Db 4 GGACAGCTUGGAUCACAC 21

RESULT 12
ADH72558
ID ADH72558 standard; DNA; 26 BP.
XX
AC ADH72558;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human probe of the invention SEQ ID NO:1454.
XX
XX human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia; ss; probe.
XX
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.
XX 07-JUN-2002; 2002US-0386796P.
XX 07-JUN-2002; 2002US-0386816P.
XX 07-JUN-2002; 2002US-0386931P.
XX 07-JUN-2002; 2002US-0386942P.
XX 07-JUN-2002; 2002US-0386971P.
XX 07-JUN-2002; 2002US-0387262P.
XX 08-JUN-2002; 2002US-0296960P.
XX 10-JUN-2002; 2002US-0387400P.
XX 10-JUN-2002; 2002US-0387535P.
XX 11-JUN-2002; 2002US-0387610P.
XX 11-JUN-2002; 2002US-0387625P.
XX 11-JUN-2002; 2002US-0387634P.
XX 11-JUN-2002; 2002US-0387668P.
XX 11-JUN-2002; 2002US-0387696P.
XX 11-JUN-2002; 2002US-0387702P.
XX 11-JUN-2002; 2002US-0387836P.
XX 11-JUN-2002; 2002US-0387859P.
XX 12-JUN-2002; 2002US-0387933P.
XX 12-JUN-2002; 2002US-0387934P.
XX 12-JUN-2002; 2002US-0387960P.
XX 12-JUN-2002; 2002US-0388022P.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zinzyme molecule of the invention

XX SQ Sequence 17 BP; 6 A; 3 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 64.0%; Score 16; DB 4; Length 17;
 Best Local Similarity 68.8%; Pred. No. 9.9e+02; Indels 0; Gaps 0;
 Matches 11; Conservative 5; Mismatches 0;

Qy 10 UUGAUCACACCCUUG 25
 :|||:|||||:|
 Db 17 TTGGATCACACCTTG 2

RESULT 14
 ABN32813/c
 ID ABN32813 standard; DNA; 60 BP.

XX AC ABN32813;

XX DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:5561.

XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 XX splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX FN WO200210449-A2.

XX PD 07-FEB-2002.

XX PP 20-JUL-2001; 2001WO-IB001903.

XX PR 28-JUL-2000; 2000US-0221607P.

XX PR 02-MAY-2001; 2001US-0287724P.

XX PA (COMP-) COMPUGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

DR

XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.

XX Example 1; SEQ ID NO 5561; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcriptome units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 60 BP; 14 A; 13 C; 16 G; 17 T; 0 U; 0 Other;

Query Match 63.2%; Score 15.8; DB 6; Length 60;
 Best Local Similarity 68.4%; Pred. No. 1.5e+03;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGCUUGAUCACACCCUUG 25
 |::|::|::|::|::|
 Db 41 ATCTTGATCACACCCATG 23

RESULT 15
 AAD36524

ID AAD36524 standard; DNA; 20 BP.

XX AC AAD36524;

XX DT 09-AUG-2002 (first entry)

XX DE Human Her-1 antisense oligonucleotide ISIS #122133.

XX KW Human; epidermal growth factor receptor; hyperproliferative disease;
 KW Her1; antisense; prophylaxis; psoriasis; phosphorothioate backbone;
 KW tumour; cancer; ss.

XX OS Homo sapiens.

XX OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/tag= a
	/mod_base= OTHER
	/note= "Phosphorothioate backbone"
modified_base	1..5
	/tag= b
	/mod_base= OTHER
	/note= "2'methoxyethyl nucleotides"
modified_base	7
	/tag= d
	/mod_base= m5C
modified_base	10

FT /*tag= e
FT /mod_base= m5c
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT 17
FT /*tag= f
FT /mod_base= m5c
FT 19
FT /*tag= g
FT /mod_base= m5c

WO200226758-A1.

04-APR-2002.

28-SEP-2001; 2001WO-US030551.

29-SEP-2000; 2000US-00676610.

(ISIS-) ISIS PHARM INC.

Bennett CF, Wyatt JR, Freier SM;

WPI; 2002-394234/42.

XX Novel antisense oligonucleotide that specifically hybridizes with and
PT inhibits nucleic acid encoding epidermal growth factor receptor, useful
FT for treating hyperproliferative disease such as cancer or psoriasis.

XX Example 19; Page 45; 169pp; English.

XX The invention relates to an antisense oligonucleotide targetted to a
CC nucleic acid molecule encoding human epidermal growth factor receptor
CC (Her1) to inhibit its expression. The antisense compounds are useful for
CC treating diseases or conditions associated with Her-1 such as
CC hyperproliferative diseases especially cancer (lung, ovarian, colon or
CC prostate cancer) and psoriasis. They are also useful as research
CC reagents, diagnostics, therapeutics, kits and prophylactically e.g. to
CC prevent or delay tumour formation. The present sequence is an antisense
CC oligonucleotide targetted to human Her-1

XX SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 61.6%; Score 15.4; DB 6; Length 20;

Best Local Similarity 76.5%; Pred.No.1.9e+03;

Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAAUAGCUUGGAUCACA 19

|||||:|:|:|:|

Db 4 GGACAGCTTGGATCACA 20

Search completed: July 30, 2005, 15:45:00

Job time : 309.77 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:01:12 ; Search time 2428.72 Seconds
(without alignments)
391.815 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25
Sequence: 1 cuggaagcuggaaccacccuug 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.4	57.6	42	8	AQ072941 EP(2)2154
C 2	14.2	56.8	46	9	AL765810 Arabidops
C 3	14.2	56.8	60	8	AZ317154 1M0035G16
C 4	14.2	56.0	45	9	AL943467 Arabidops
C 5	13.8	55.2	55	9	CL528471 ASV13H02.
C 6	13.6	54.4	34	9	AL942366 Arabidops
C 7	13.6	54.4	51	8	BH908280 SALK 0469
C 8	13.6	54.4	58	1	AA918654 ol67f12.8
C 9	13.4	53.6	36	2	BB617639
C 10	13.4	53.6	36	8	AZ800990
C 11	13.2	52.8	25	8	BH814737
C 12	13.2	52.8	42	8	BH630486
C 13	13.2	52.8	51	8	AZ771156
C 14	13.2	52.8	59	1	AA207740
C 15	13.2	52.8	59	8	AZ395181
C 16	13	52.0	43	1	AA676294
C 17	13	52.0	56	9	AL763703
C 18	12.8	51.2	36	4	BG538454
C 19	12.8	51.2	41	9	AL762995
C 20	12.8	51.2	43	1	A1097835
C 21	12.8	51.2	43	1	A1491879
C 22	12.8	51.2	43	8	BH901304
C 23	12.8	51.2	49	1	AA168179
C 24	12.8	51.2	49	9	AL765094 Arabidops

25	12.8	51.2	50	7	H60434
C 26	12.8	51.2	52	4	BJ000348
C 27	12.8	51.2	52	9	CR164369
C 28	12.8	51.2	56	1	AL777445
C 29	12.8	51.2	57	8	CC458457
C 30	12.8	51.2	59	9	CR247136
C 31	12.6	50.4	28	8	AZ782057
C 32	12.6	50.4	31	2	AV962471
C 33	12.6	50.4	34	7	N63645
C 34	12.6	50.4	35	2	BF036425
C 35	12.6	50.4	43	9	CG869098
C 36	12.6	50.4	51	8	BH856117
C 37	12.6	50.4	56	7	H69956
C 38	12.6	50.4	57	9	CG774043
C 39	12.6	50.4	58	8	AZ783926
C 40	12.6	50.4	60	6	CD917506
C 41	12.4	49.6	37	8	AZ423769
C 42	12.4	49.6	50	1	AU105134
C 43	12.4	49.6	52	4	BJ000348
C 44	12.4	49.6	52	7	CN922922
C 45	12.4	49.6	53	6	CB353071

ALIGNMENTS

RESULT 1
AQ072941/c
LOCUS
DEFINITION
EP(2)2154 Drosophila melanogaster EP line Drosophila melanogaster
Genomic Sequence recovered from Both 5' and 3' ends of P element,
genomic survey sequence.
ACCESSION
AQ072941
VERSION
AQ072941.1 GI:3403392
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
Liao, G.-C., Rehm, E.J. and Rubin, G.M.
Insertion site preferences of the P transposable element in
Drosophila melanogaster
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
JOURNAL
MEDLINE
20202638
PUBMED
10716700
COMMENT
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 7 in the 42 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

1. .42

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone lib="Drosophila melanogaster Ep line"

/note="Inverse PCR was performed on Drosophila

melanogaster strains each of which contains a single Ep

transposable element insertion. (The generation of these

insertion strains is described in Rorth P, Szabo K, Bailey

A, Lavery T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes


```

/strain="Columbia_0"
/db_xref="taxon:3702"
/clone="GK-274F03-015094"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AU37514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

```

T-DNA derived sequences were removed."

Query Match	56.0%	Score 14;	DB 9;	Length 45;
Best Local Similarity	54.5%;	Pred. No. 7.8e+04;		
Matches 12;	Conservative	5;	Mismatches 5;	Indels 0;
Matches	12;	Conservative	5;	Indels 0;

21 CCGGATTGCTGGGATCACA 39

AL943467
LOCUS
AL943467 45 bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-274F03-015094,
genomic survey sequence.

VERSION AL943467.1 GI:24400065
KEYWORDS GSS.

SOURCE	ORGANISM
Arabidopsis thaliana (thale cress)	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
TITLE GABI-Rat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis

thaliana

**JOURNAL
BIOINFORMATICS 19 (11), 1441-1442 (2003)
MEDLINE
22755829**

PUBMED REFERENCE	12874060 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.

TITLE An *Arabidopsis thaliana* T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE	23117147
PUBMED	14756321
REFERENCE	3

AUTHORS	Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.
TITLE	High-throughput generation of sequence indexes from T-DNA

JOURNAL
PUBMED
REFERENCE 4 (bases 1 to 45)
Biotechniques 35 (6), 1164-1168 (2003)
mutagenized *Arabidopsis thaliana* lines
14682050

REFERENCES
AUTHORS
TITLE
JOURNAL

COMMENT
Zuchtungsforſchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This ſequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone

t14c8. Details on the protocols used for generation of the sequences are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat

project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

```

FEATURES
source
1. .45
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"

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www.officemanager.com

```

Db      12 CTGAGTAGCTGGGACACAGGCATG 36

RESULT 6
LOCUS   AL942366
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-265D06-014998, genomic survey sequence.
ACCESSION AL942366
VERSION   AL942366.1
KEYWORDS  GI:24398964
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS  Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
TITLE    GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL  Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE  22755829
PUBMED   12874060
AUTHORS  Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE    An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL  Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE  23117147
PUBMED   14756321
AUTHORS  Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.
TITLE    High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL  BioTechniques 35 (6), 1164-1168 (2003)
MEDLINE  14682050
PUBMED   14682050
AUTHORS  Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
TITLE    Direct Submission
JOURNAL  Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT  This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Atlg48900. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
    Location/Qualifiers
        1..34
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /strain="Columbia 0"
            /db_xref="taxon:3702"
            /clone="GK-265D06-014998"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /ecotype="Col-0"
            /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match      54.4%; Score 13.6; DB 9; Length 34;
Best Local Similarity 55.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

RESULT 7
LOCUS   BH908280
DEFINITION Arabidopsis thaliana T-DNA insertion lines
ACCESSION BH908280
VERSION   BH908280.1
KEYWORDS  GI:22721213
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE    A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL  Unpublished (2001)
COMMENT  Contact: Joseph R. Ecker
          Salk Institute Genomic Analysis Laboratory (SIGNAL)
          The Salk Institute for Biological Studies
          10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
          Tel: 858 453 4100 x1752
          Fax: 858 558 6379
          Email: eckergsalk.edu
          This is single pass sequence recovered from the left border of T-DNA.

FEATURES
    Location/Qualifiers
        1..51
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /ecotype="Col-0"
            /db_xref="taxon:3702"
            /clone="SALK_046972.17.10.x"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      54.4%; Score 13.6; DB 8; Length 51;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      4 GAUAGCUUGGUAUACACCCU 23
        ||: ||: ||: ||: ||:
Db      14 GATCTCTTCGATCAACCCCT 33

RESULT 8
LOCUS   AA918654
DEFINITION Arabidopsis thaliana T-DNA insertion lines
ACCESSION AA918654
VERSION   AA918654.1
KEYWORDS  GI:3058544
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS  Ol67f12.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534703
TITLE    similar to TR:Q99622 Q99622 CHROMOSOME 12P13 SEQUENCE; HTGS PHASE 3, COMPLETE SEQUENCE.; mRNA sequence.

FEATURES
    Location/Qualifiers
        58 bp mRNA linear EST 10-JUN-1998
        ol67f12.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534703
        similar to TR:Q99622 Q99622 CHROMOSOME 12P13 SEQUENCE; HTGS PHASE 3, COMPLETE SEQUENCE.; mRNA sequence.

ORIGIN
Query Match      54.4%; Score 13.6; DB 9; Length 34;
Best Local Similarity 55.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```


Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 58)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 519 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source
1..58
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1534703"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Kid3"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 54.4%; Score 13.6; DB 1; Length 58;
Best Local Similarity 70.0%; Pred. No. 1.3e+05;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGAUAGCGTGGATCACTCC 23
||| ||| :||| |||
Db 4 GGAUAGCGTGGATCACTCC 23

RESULT 9
BE617639
LOCUS
DEFINITION
60144159071 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845711 3', mRNA sequence.

ACCESSION
BE617639
VERSION
KEYWORDS
EST.
Homo sapiens (human)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 36)

TITLE
NIH-MGC <http://mgs.nci.nih.gov/>.

JOURNAL
National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Htp: L1AM9557 row: c column: 24
High quality sequence start: 18
High quality sequence stop: 36.

FEATURES
Location/Qualifiers
source
1..36

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3845711"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 53.6%; Score 13.4; DB 2; Length 36;
Best Local Similarity 56.5%; Pred. No. 1.5e+05;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCU 23
||| ||| :||| |||
Db 7 CGGACGAGATTGGTCCACCT 29

RESULT 10

AZ800990

LOCUS

DEFINITION

2M0059H15F Mouse 10kb plasmid UUGCLM library Mus musculus genomic

clone UUGC2M0059H15 F, genomic survey sequence.

ACCESSION

AZ800990

VERSION

GI:12953313

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 36)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.;

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: H column: 15

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 36.

Location/Qualifiers

source
1..36

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0059H15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/note="vector: PMD42nv; Purified genomic DNA from M.

AA207740/c
LOCUS
DEFINITION
AA207740 59 bp mRNA linear EST 12-MAR-1997
mv78h05.r1 GuayWoodford Beiler mouse kidney day 7 Mus musculus cDNA
clone IMAGE:661209 5', similar to gb:X13661 Mouse mRNA for
elongation factor 1-alpha (MOUSE);, mRNA sequence.
AA207740 GI:1804254
AA207740.1 GI:1804254
EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bukaryaota; Metazoa; Chordata; Vertebrata; Euteleostomi;
1 (bases 1 to 59)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:407057
Trace considered overall poor quality
Seq primer: -28m13 rev1 ET from Amersham

```

FEATURES
  source
    1. .59
      Location/Qualifiers
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="IMAGE:661209"
        /tissue_type="kidney"
        /dev_stage="juvenile (7 days old)"
        /lab_host="SOLR (kanamycin resistant)"
        /clone_lib="GuayWoodford Beller mouse kidney day 7"
        /notes="Organ: kidney; Vector: pBluescript SK-; Site 1:
        ECGRI; Site 2: XhoI; Cloned unidirectionally. Primer:
        Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
        ~5' adaptor sequence: 5' GAATTCGCACGAG 3' ~3' adaptor
        sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Library provided
        by Lisa Guay-Woodford."

ORIGIN
Query Match          52.8%;   Score 13.2;   DB 1;   Length 59;
Best Local Similarity 66.7%;   Pred. No. 1.9e+05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      5  AUAAGCTUGGAUACACACC 22
      | |||::||: |||||
Db      46  ACAGCTTTGATGACACC 29

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RESULT 15	AZ395181	59'bp	DNA	linear	GSS 03-OCT-2000
LOCUS	AZ395181				
DEFINITION	1M0159M03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0159M03 F, Genomic survey sequence.				
ACCESSION	AZ395181				
VERSION	AZ395181.1				
KEYWORDS	GI:10510253				
SOURCE	GSS.				
ORGANISM	Mus musculus (house mouse)				
	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				

REFERENCE 1 (bases 1 to 59)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0159 row: M column: 03
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 59.
FEATURES
source
1..59
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0159W03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 52.8%; Score 13.2; DB 8; Length 59;
Best Local Similarity 61.1%; Pred. No. 1.9e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 UGGAUAGCUGGAUACA 19
| : ||| : ||| : ||
Db 7 TGAATAGCTGGGATTACA 24

Search completed: July 30, 2005, 18:20:42
Job time : 2432.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:05:52 ; Search time 87.8378 Seconds
(without alignments)
465.710 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

Sequence: 1 cuggaagcuggaucacacccuug 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	61.6	20	3	US-09-676-610B-38
C 2	14.4	57.6	17	3	US-08-985-162-100
C 3	14.4	57.6	17	3	US-09-401-083-100
4	14.2	56.8	31	1	US-08-240-547-3
C 5	14	56.0	40	3	US-09-485-737B-12
C 6	14	56.0	40	4	US-10-071-485-12
C 7	14	56.0	40	4	US-08-750-703-10
C 8	13.6	54.4	25	4	US-09-396-196G-75584
9	13.6	54.4	25	4	US-09-396-196G-94761
10	13.6	54.4	25	4	US-08-513-968-39
C 11	13.4	53.6	18	2	US-09-205-860-53
C 12	13.4	53.6	25	4	US-09-396-196G-23284
13	13.4	53.6	25	4	US-09-396-196G-124476
14	13.4	53.6	40	5	PCT-US91-00909-10
C 15	13.4	53.6	43	5	PCT-US91-00909-13
16	13.4	53.6	56	4	US-09-513-999C-18929
C 17	13.4	53.6	60	3	US-08-729-601A-41
C 18	13.2	52.8	47	4	US-09-422-978-1184
C 19	13.2	52.8	50	1	US-08-207-901-66
C 20	13.2	52.8	60	1	US-08-484-182-177
C 21	13	52.0	25	4	US-09-396-196G-113155
22	13	52.0	26	3	US-08-640-737-13
C 23	13	52.0	27	3	US-09-020-846-32
C 24	13	52.0	33	1	US-08-417-476-21
C 25	13	52.0	34	3	US-09-162-021B-18
C 26	13	52.0	39	1	US-08-324-243-25
C 27	13	52.0	39	1	US-08-532-390-25

C 28	13	52.0	39	3	US-08-717-294-25	Sequence 25, Appl
C 29	13	52.0	39	5	PCT-US95-11511-25	Sequence 25, Appl
C 30	13	52.0	60	5	PCT-US95-11985A-9	Sequence 9, Appl
C 31	12.8	51.2	19	4	US-08-983-605-168	Sequence 168, App
C 32	12.8	51.2	20	4	US-09-422-978-10858	Sequence 10858, A
C 33	12.8	51.2	23	3	US-08-276-968A-28	Sequence 28, Appl
C 34	12.8	51.2	25	4	US-09-274-752D-16	Sequence 16, Appl
C 35	12.8	51.2	25	4	US-09-396-196G-76462	Sequence 76462, A
C 36	12.8	51.2	26	4	US-09-439-813-4	Sequence 4, Appl
C 37	12.8	51.2	26	4	US-09-439-813-6	Sequence 6, Appl
C 38	12.8	51.2	28	3	US-09-012-097A-21	Sequence 21, Appl
C 39	12.8	51.2	29	4	US-09-791-105B-28	Sequence 28, Appl
C 40	12.8	51.2	33	3	US-09-461-697-134	Sequence 134, App
C 41	12.8	51.2	36	4	US-09-978-758-17	Sequence 17, Appl
C 42	12.8	51.2	40	3	US-08-961-083-297	Sequence 297, App
C 43	12.8	51.2	40	4	US-09-536-784-297	Sequence 297, App
C 44	12.8	51.2	48	4	US-09-591-466C-10	Sequence 10, Appl
C 45	12.8	51.2	50	1	US-08-207-901-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-09-676-610B-38
; Sequence 38, Application US/09676610B
; Patent No. 6444465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676.610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-676-610B-38

Query Match 61.6%; Score 15.4; DB 3; Length 20;
Best Local Similarity 76.5%; Pred. No. 4.4e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy	3	GGUAGCUUGAUCACA	19
		:	
Db	4	GGACAGCTTGGATCACA	20

RESULT 2

US-08-985-162-100/c
; Sequence 100, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggan, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

```
/
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq for Windows 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/985,162
/ FILING DATE: 04 December 1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/036,476
/ FILING DATE: 31 January 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 230/107
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 100:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-985-162-100

Query Match 57.6%; Score 14.4; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 AUAGCUUGAUCACAC 20
DB 17 ACAGCTTGGATCACAC 2

RESULT 3
US-09-401-063-100/c
/ Sequence 100, Application US/09401063
/ Patent No. 6623962
/ GENERAL INFORMATION:
/ APPLICANT: Akhtar, Saghir
/ APPLICANT: Fell, Patricia
/ TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
/ TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
/ TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
/ TITLE OF INVENTION: FACTOR RECEPTORS
/ NUMBER OF SEQUENCES: 1877
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq for Windows 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/401,063
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/985,162
/ FILING DATE: 04 December 1997
```

```
/
/ APPLICATION NUMBER: 60/036,476
/ FILING DATE: 31 January 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 230/107
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 100:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-401-063-100

Query Match 57.6%; Score 14.4; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 AUAGCUUGAUCACAC 20
DB 17 ACAGCTTGGATCACAC 2

RESULT 4
US-08-240-547-3
/ Sequence 3, Application US/08240547
/ Patent No. 5527669
/ GENERAL INFORMATION:
/ APPLICANT: Resnick, Robert M.
/ APPLICANT: Young, Karen K.Y.
/ TITLE OF INVENTION: Primers and Probes for Detection of
/ TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hoffmann-La Roche Inc.
/ STREET: 340 Kingsland Street
/ CITY: Nutley
/ STATE: NJ
/ COUNTRY: U.S.A.
/ ZIP: 07110-1199
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/240,547
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/918,944
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sias Ph.D., Stacey R.
/ REGISTRATION NUMBER: 32,630
/ REFERENCE/DOCKET NUMBER: 8586
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (510) 814-2863
/ TELEFAX: (510) 814-2977
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/
US-08-240-547-3

Query Match 56.8%; Score 14.2; DB 1; Length 31;
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Best Local Similarity 63.2%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 7 AGCUUGAUCACACCCUUG 25
|||:|||||:|
Db 4 AGCTTAGATCACTCCCTG 22

RESULT 5
US-09-485-737B-12/c
; Sequence 12, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: GENOMIC

US-09-485-737B-12

Query Match 56.0%; Score 14; DB 3; Length 40;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGAUCACACCCU 23
|||:|||||:|
Db 34 TGGATGGTTGGATCAACACCT 13

RESULT 6
US-10-071-485-12/c
; Sequence 12, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:

US-09-544-776-3

Query Match 56.0%; Score 14; DB 3; Length 40;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGAUCACACCCU 23
|||:|||||:|
Db 34 TGGATGGTTGGATCAACACCT 13

RESULT 7
US-08-750-703-10/c
; Sequence 10, Application US/08750703
; Patent No. 5891633
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Frank J.; Idle, Jeffrey R.
; TITLE OF INVENTION: DEFECTS IN DRUG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Ave.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,703
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07605
; FILING DATE: 16-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dorothy R. Auth
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4196PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; NAME/KEY: F4 primer
; LOCATION:
; OTHER INFORMATION: Primer used for CYP2A6
; OTHER INFORMATION: genotyping.

US-08-750-703-10

Query Match 56.0%; Score 14; DB 2; Length 57;
Best Local Similarity 59.1%; Pred. No. 2.4e+03;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CUGAUGAGCUUGAUCACACCC 22
|||:|||||:|
Db 41 CTGCCTAGCTTGGACACAGCC 20

RESULT 8
US-09-396-196G-75584/c
; Sequence 75584, Application US/09396196G

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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-75584

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 55.0%; Pred. No. 3.4e+03;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 6 UAGCUUGGAUCACACCCUUG 25
Db :|||||:|||||:|:|

RESULT 9
US-09-396-196G-94761
; Sequence 94761, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-94761

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 55.0%; Pred. No. 3.4e+03;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 6 UAGCUUGGAUCACACCCUUG 25
Db :|||||:|||||:|:|

RESULT 10
US-08-513-968-39
; Sequence 39, Application US/08513968
; Patent No. 611413
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
```

```
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..56
US-08-513-968-39

Query Match 54.4%; Score 13.6; DB 3; Length 56;
Best Local Similarity 55.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CUGGAUGCUUGGAUCACAC 20
Db :|||||:|||||:|:|
30 CTGGATAGGTGGTTAGAC 49

RESULT 11
US-09-205-860-53/C
; Sequence 53, Application US/09205860
; Patent No. 5981732
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
; FILE REFERENCE: RTS-0031
; CURRENT APPLICATION NUMBER: US/09/205,860
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 53
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-860-53

Query Match 53.6%; Score 13.4; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 4e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 CUGGAUAGCUUGGAU 15
:||||| |::|||:
Db 16 CTGGATACCTGGAT 2

RESULT 12
US-09-396-196G-23284
; Sequence 23284, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100, 678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23284
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-23284

Query Match 53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 47.8%; Pred. No. 4.2e+03;
Matches 11; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGGAUCACACCCUU 24
:||||| |::|||:
Db 2 TGCATTGCTAGTGCACAGCCTT 24

RESULT 13
US-09-396-196G-124476
; Sequence 124476, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100, 678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124476
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124476

Query Match 53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.3%; Pred. No. 4.2e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 11 UGGAUCACACCCUUG 25
:||||| |::|||:
Db 4 TGGATCACACCCGTG 18

RESULT 14
PCT-US91-00909-10
; Sequence 10, Application PC/TUS9100909
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; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: United States
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00909
; FILING DATE: 19910208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.408PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US91-00909-10

Query Match 53.6%; Score 13.4; DB 5; Length 40;
Best Local Similarity 52.2%; Pred. No. 4.5e+03;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGGAUCACACCCUU 24
:||||| |::|||:
Db 11 TGAGTAGCAACGATCATACCTT 33

RESULT 15
PCT-US91-00909-13/c
; Sequence 13, Application PC/TUS9100909
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: United States
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00909
; FILING DATE: 19910208
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.408PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US91-00909-13

Query Match      53.6%; Score 13.4; DB 5; Length 43;
Best Local Similarity 52.2%; Pred.No. 4.5e+03;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      2 UGGAUAGCUUGGAUCACACCCUU 24
Db      28 TGAGTAGCAACGATCATACCTT 6
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Search completed: July 30, 2005, 18:25:12
Job time : 89.8378 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:54:37 ; Search time 718.243 Seconds
(without alignments)
1686.588 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25
Sequence: 1 caacuacaggaucacagauagccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1981570

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	16.2	64.8	42	6	A32288 DNA probe (
C 3	16.2	64.8	59	6	A32049 DNA probe (
C 4	16.2	64.8	59	6	A32067 DNA probe (
C 5	16.2	64.8	60	6	CQ544937 Sequence
C 6	16.2	64.8	17	6	AX215126 Sequence
C 7	15.6	62.4	33	6	AR365650 Sequence
C 8	15.6	62.4	33	6	AR365669 Sequence
C 9	15.6	62.4	34	6	AR365637 Sequence
C 10	15.6	62.4	39	6	AR365666 Sequence
C 11	15.4	61.6	20	6	BD134588
C 12	15.0	60.0	17	6	AX215125
C 13	15.0	60.0	17	6	AX216000 Sequence
C 14	15.0	60.0	60	6	CQ536812 Sequence
C 15	14.8	59.2	23	6	AX539243 Sequence
C 16	14.8	59.2	38	6	AR254609 Sequence
C 17	14.6	58.4	42	6	ES9732 Method for
C 18	14.4	57.6	21	6	BD012596 Human cyt
C 19	14.4	57.6	51	11	EX088624 Arabidops

20	14.2	56.8	60	6	CQ537523	CQ537523 Sequence
c 21	14	56.0	17	6	AX217202	AX217202 Sequence
c 22	14	56.0	20	6	AX247495	AX247495 Sequence
23	14	56.0	24	6	BD073932	BD073932 RTD recep
24	14	56.0	26	6	AX099785	AX099785 Sequence
25	14	56.0	32	6	AX786475	AX786475 Sequence
c 26	14	56.0	34	6	AR365647	AR365647 Sequence
27	14	56.0	39	6	AR365667	AR365667 Sequence
c 28	14	56.0	48	6	BD222069	BD222069 SH2 domai
c 29	14	56.0	48	6	AR179726	AR179726 Sequence
c 30	14	56.0	54	6	AX927857	AX927857 Sequence
c 31	14	56.0	54	8	AJ719032	AJ719032 Nicotiana
32	14	56.0	60	6	BD175864	BD175864 A method
33	14	56.0	60	6	CQ547543	CQ547543 Sequence
34	14	56.0	60	6	AX404737	AX404737 Sequence
c 35	13.8	55.2	22	6	ES9733	ES9733 Method for
c 36	13.8	55.2	27	6	AR564905	AR564905 Sequence
37	13.8	55.2	36	6	AR011196	AR011196 Sequence
38	13.8	55.2	36	6	ES4595	ES4595 Herpesvirus
39	13.8	55.2	36	6	117834	117834 Sequence 64
40	13.8	55.2	59	6	AR236928	AR236928 Sequence
c 41	13.8	55.2	60	6	CQ539376	CQ539376 Sequence
c 42	13.8	55.2	60	6	CQ543926	CQ543926 Sequence
c 43	13.8	55.2	60	6	CQ548098	CQ548098 Sequence
c 44	13.6	54.4	25	6	AR435430	AR435430 Sequence
c 45	13.6	54.4	25	6	AR435431	AR435431 Sequence

ALIGNMENTS

RESULT 1
A32068/c
LOCUS A32068 42 bp DNA linear PAT 08-DEC-1995
DEFINITION DNA probe (A.salmonicida) from patent EP0395292.
ACCESSION A32068
VERSION A32068.1 GI:1249523
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Barry,T.G., Gannon,B.X. and Powell,R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 43 31-OCT-1990;
IRELAND; Powell, Richard; Gannon, Bernard Francis Xavier; BIORESEARCH
GERARD; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;
Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard;
Gannon, Bernard Francis Xavier; BOLAS (trading as BioResearch
Ireland) - The Irish Science and Technology Agency; Powell,
Richard; UNIVERSITY COLLEGE GALWAY

FEATURES
Location/Qualifiers
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1..42
/organism="synthetic construct"
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ORIGIN

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Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CUUCAGGAUUCACGAUAGCC 24

Db 28 CTACAGGATTCACAGATGTC 8

RESULT 2

A32288/c
LOCUS A32288 42 bp DNA linear PAT 08-DEC-1995
DEFINITION DNA probe (A.salmonica) from patent EP0395292.
ACCESSION A32288

```

VERSION A32288.1 GI:1249529
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 42)
AUTHORS Barry, T.G., Gannon, B.X. and Powell, R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 49 31-OCT-1990;
IRELAND; Powell, Richard; Gannon, Bernard Francis Xavier; BIORESEARCH
Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;
Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard;
Gannon, Bernard Francis Xavier; EOLAS (trading as BioResearch
Ireland) - The Irish Science and Technology Agency; Powell,
Richard; UNIVERSITY COLLEGE GALWAY
FEATURES
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Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 CUUCAGGAUCCAGAUAGCC 24
Db 28 CTCAGGATTCAGACATGTC 8
RESULT 3
A32049/c
LOCUS DNA probe (A.hydrophila) from patent EP0395292.
DEFINITION A32049
ACCESSION A32049.1 GI:1249504
VERSION A32049.1
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 59)
AUTHORS Barry, T.G., Gannon, B.X. and Powell, R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 24 31-OCT-1990;
IRELAND; Powell, Richard; Gannon, Bernard Francis Xavier; BIORESEARCH
Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;
Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard;
Gannon, Bernard Francis Xavier; EOLAS (trading as BioResearch
Ireland) - The Irish Science and Technology Agency; Powell,
Richard; UNIVERSITY COLLEGE GALWAY
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Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 CUUCAGGAUCCAGAUAGCC 24
Db 28 CTCAGGATTCAGACATGTC 8
RESULT 4
A32067/c
LOCUS DNA probe (A.hydrophila) from patent EP0395292.
DEFINITION A32067
ACCESSION A32067.1 GI:1249522
VERSION A32067.1
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 59)
AUTHORS Barry, T.G., Gannon, B.X. and Powell, R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 42 31-OCT-1990;
IRELAND; Powell, Richard; Gannon, Bernard Francis Xavier; BIORESEARCH
Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;
Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard;
Gannon, Bernard Francis Xavier; EOLAS (trading as BioResearch
Ireland) - The Irish Science and Technology Agency; Powell,
Richard; UNIVERSITY COLLEGE GALWAY
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Query Match 64.8%; Score 16.2; DB 6; Length 59;
Best Local Similarity 66.7%; Pred. No. 4.7e+03;
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QY 4 CUUCAGGAUCCAGAUAGCC 24
Db 28 CTCAGGATTCAGACATGTC 8
RESULT 5
CQ544937/c
LOCUS Sequence 14572 from Patent WO0210449.
DEFINITION CQ544937
ACCESSION CQ544937.1 GI:41511201
VERSION CQ544937.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 14572 07-FEB-2002;
Compugen Inc. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Best Local Similarity 57.1%; Pred. No. 4.7e+03;
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QY 5 UUCAGGAUCCAGAUAGCC 25
Db 23 TTCAGGATTCAGATATCC 3
RESULT 6
AX215126/c
LOCUS Sequence 568 from Patent WO0159103.
DEFINITION AX215126
ACCESSION AX215126.1 GI:15525169
VERSION AX215126.1
KEYWORDS

```

[illegible]

```

DEFINITION Dioxin receptor gene and utilization thereof.
ACCESSION BD134588
VERSION BD134588.1 GI:23229533
KEYWORDS JP 2002045188-A/5
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Oe,N.
TITLE Dioxin receptor gene and utilization thereof
JOURNAL Patent: JP 2002045188-A 5 12-FEB-2002;
COMMENT SUMITOMO CHEMICAL CO LTD
PN OS Artificial Sequence
PD JP 2002045188-A/5
PP 04-AUG-2000 JP 2000236762
PI NORIHISA OE
PC C12N15/09,C07K14/705,C12N5/10,C12N7/00,C12P21/02,C12Q1/02, PC
GO1N33/566,
PC GO1N33/68// (C12N5/10,C12R1:93), (C12P21/02,C12R1:93), C12N15/00,
C12N5/00,
PC (C12N5/00,C12R1:93)
CC Designed oligonucleotide primer for PCR
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
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Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAACUUCAGGUAUCCAG 17
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Db 17 CAACTTCAGGATCCCG 1

RESULT 12
AX215125/c
LOCUS AX215125 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 567 from Patent WO0159103.
ACCESSION AX215125
VERSION AX215125.1 GI:15525168
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 567 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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Best Local Similarity 73.3%; Pred. No. 1.8e+04;
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QY 3 ACUUCAGGAUCCAGAUGCC 25
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Db 8 ACATCAGGTTCCAGACTAGCC 30

RESULT 13
AX216000/c
LOCUS AX216000 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1442 from Patent WO0159103.
ACCESSION AX216000
VERSION AX216000.1 GI:15526043
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1442 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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QY 10 GAUUCAGAUUAGGCC 24
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Db 15 GATTCAGATATGCC 1

RESULT 14
CQ536812
LOCUS CQ536812 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6447 from Patent WO0210449.
ACCESSION CQ536812
VERSION CQ536812.1 GI:41503076
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 6447 07-FEB-2002;
Compugen Inc. (US)
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Best Local Similarity 65.2%; Pred. No. 1.9e+04;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 ACUUCAGGAUCCAGAUGCC 25
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Db 8 ACATCAGGTTCCAGACTAGCC 30

RESULT 15
AX539243
LOCUS AX539243 23 bp DNA linear PAT 23-NOV-2002
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Best Local Similarity 73.3%; Pred. No. 1.8e+04;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 11 AUUCAGGAUCCAGGCC 25
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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
480.857 Million cell updates/sec

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	25	100.0	25	AAC64408	Human Nog
C 2	16.2	64.8	60	ABN41824	Human spl
C 3	16	64.0	17	ABK00568	Human NOG
C 4	16	64.0	41	ADL64316	Human sin
C 5	15.8	63.2	19	ADR79899	Human apo
C 6	15.8	63.2	19	ADR77241	Human apo
C 7	15.8	63.2	19	ADR80185	Human apo
C 8	15.8	63.2	19	ADR76955	Human apo
C 9	15.8	63.2	20	AAQ10833	Pneumocys
C 10	15.6	62.4	34	AAT42447	Probe 148
C 11	15.6	62.4	41	ABL40078	Phosphoen
C 12	15.6	62.4	41	ABL40079	Phosphoen
C 13	15.4	61.6	20	ABL54676	Cricetulu
C 14	15	60.0	17	ABK00567	Human NOG
C 15	15	60.0	17	ABK01442	Human NOG
C 16	15	60.0	60	ABN33699	Human spl
C 17	14.8	59.2	23	ABN33699	Human mul
C 18	14.8	59.2	38	AAT14558	Cytotacti
C 19	14.6	58.4	24	ADN76060	C japonic
C 20	14.6	58.4	34	ADN7188	Bacillus

C 21	14.6	58.4	42	3	AAA62887	Forward P
C 22	14.6	58.4	45	2	AAQ66143	DNA-polym
C 23	14.6	58.4	47	12	ADN11426	Adn11426 FLJ14528
C 24	14.4	57.6	21	5	AAF92390	T7 clone
C 25	14.4	57.6	32	1	AAQ92390	Sequence
C 26	14.4	57.6	33	12	ADJ63889	Plant lip
C 27	14.4	57.6	41	12	ADL64169	Human sin
C 28	14.2	56.8	29	3	AZ288270	Sec B nuc
C 29	14.2	56.8	50	6	ABZ00890	Human leu
C 30	14.2	56.8	51	13	ADR35716	Human nic
C 31	14.2	56.8	51	13	ADR35715	Human nic
C 32	14.2	56.8	51	13	ADR35713	Human nic
C 33	14.2	56.8	51	13	ADR35714	Human nic
C 34	14.2	56.8	60	6	ABN34410	Human spl
C 35	14	56.0	17	4	ABK02644	Human NOG
C 36	14	56.0	20	4	ABL58226	Virulence
C 37	14	56.0	24	2	AAQ25095	PCR prime
C 38	14	56.0	26	4	AAQ03304	Reverse p
C 39	14	56.0	27	2	AAQ28212	Tumour an
C 40	14	56.0	27	10	ADC82787	DNA seque
C 41	14	56.0	32	8	ACC43414	PCR prime
C 42	14	56.0	34	2	AAQ10833	Pneumocys
C 43	14	56.0	34	2	AAT42445	Probe 149
C 44	14	56.0	41	6	ABL40078	Phosphoen
C 45	14	56.0	47	6	ABK52807	Human pro

ALIGNMENTS

RESULT 1
AAC64408
ID AAC64408 standard; RNA; 25 BP.
XX
AC AAC64408;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:4.
KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
KW stress-phosphorylated endoplasmic reticulum protein; cytoskeletal;
KW gene therapy; cell growth; cellular stress response; neuron growth;
KW regulator of oxidative stress; inhibitor of neurite outgrowth;
KW axon regeneration; diagnosis; cancer; identification; antisense;
KW phosphorothioate; ss.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FT modified_base 1..25
FT /*tag= a
FT /note= "phosphorothioate linkages"

XX WO2000060083-A1.

XX 12-OCT-2000.

XX 07-APR-2000; 2000WO-US009383.

XX 08-APR-1999; 99US-0128372P.

XX 21-JUN-1999; 99US-0140331P.

XX (CHIR) CHIRON CORP.

XX Wei D, Halenbeck R, Williams LT;

XX WPI; 2000-665007/64.

XX Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

```

PS Claim 25; Page 32; 68pp; English.
XX
CC The present invention describes a human stress-phosphorylated endoplasmic
CC reticulum protein, designated Nogo B. Nogo B has cytoskeletal activity and
CC is a modulator of the storage and exchange of calcium, cell growth and
CC cellular stress response. It can: regulate oxidative stress; inhibit
CC neurite outgrowth, neuron growth and axon regeneration. Nogo B
CC polypeptides and polynucleotides are useful for modulating stress levels
CC and cellular stress-response, cell growth and viability, diagnosis and
CC treatment of cancer, malignant growth and other Nogo B related diseases.
CC Nogo B polypeptides are also useful to screen combinatorial libraries to
CC identify agonist or antagonist. Antibodies against Nogo B polypeptides
CC are useful for affinity chromatography and distinguishing Nogo B
CC polypeptides. The present sequence represents a human Nogo B
CC phosphothioate antisense oligonucleotide from the present invention
XX
SQ Sequence 25 BP; 7 A; 8 C; 4 G; 0 T; 6 U; 0 Other;
Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGCC 25
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Db 1 CAACUUCAGGAUCCAGAUAGCC 25

RESULT 2
ABN41824/c
ID ABN41824 standard; DNA; 60 BP.
AC
AC ABN41824;
XX
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:14572.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
XX
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 14572; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC )transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or

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CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 12 A; 13 C; 13 G; 22 T; 0 U; 0 Other;
Query Match 64.8%; Score 16.2; DB 6; Length 60;
Best Local Similarity 57.1%; Pred. No. 9e+02;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 5 UUCAGGAUCCAGAUAGCC 25
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Db 23 TTCACGGTTCAGATATCCC 3

RESULT 3
ABK00568/c
ID ABK00568 standard; RNA; 17 BP.
XX
AC ABK00568;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human Nogo Hammerhead Ribozyme #568.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zynzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX
XX 28-FEB-2000; 2000US-0185516P.
XX
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (BLAY/) BLATT L.
XX
XX (MCSW/) MCSWIGGEN J.
XX
XX (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite

```

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 XX central nervous system injury.

PS Claim 88; Page 75; 200pp; English.

CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NIGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with an NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NIGO-
 CC targeting nucleic acid is used to cleave RNA of the NIGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NIGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NIGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NIGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NIGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention

XX Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 64.0%; Score 16; DB 4; Length 17;
 Best Local Similarity 75.0%; Pred. No. 9.4e+02;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAUUCAGCAUAUUGCCC 25

Db ||:|||||:|||||
 16 GATTCAGATATGCC 1

RESULT 4

ADL64316/c

XX ADL64316 standard; DNA; 41 BP.

XX AC ADL64316;

XX 20-MAY-2004 (first entry)

DE Human single nucleotide polymorphism (SNP) #239.

XX ss: human; single nucleotide polymorphism: SNP;
 KW Cl S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;
 KW meprin A beta protein; aminopeptidase P-like protein; XPN-PEPL;
 KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPIB;
 KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;
 KW angioedema; angioedema-like disorder; paternity testing;
 KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
 KW coronary artery disease; arteriosclerosis; hypersensitivity;
 KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
 KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
 KW cancer; ANPEP.

XX Homo sapiens.

OS

XX

PN US2004033582-A1.

XX 19-FEB-2004.

XX 03-JUN-2003; 2003US-00453827.

XX 03-JUN-2002; 2002US-0384980P.

XX (EDMO//) EDMONDS M.

XX (HUIL//) HUI L.

XX (PERR//) PERRONE M.

XX (POWE//) POWELL J R.

XX (RAMA//) RAMANATHAN C S.

XX (SWAN//) SWANSON B. Z.

XX (TSUC//) TSUCHIHASHI Z.

XX (ZERB//) ZERBA K.

XX Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;
 PI Tsuchihashi Z, Zerba K;

XX WPI; 2004-180052/17.

XX New nucleic acid comprising a single nucleotide polymorphism at a
 PT specific location, useful in paternity testing, genetic analysis or
 PT diagnosing, preventing or treating cardiovascular diseases e.g.
 PT angioedema or angina pectoris.

XX Claim 3; SEQ ID NO 239; 376pp; English.

XX The invention relates to an isolated nucleic acid (I) derived from a
 CC human gene encoding a protein, such as the Cl, S subcomponent protein
 CC (C1S), the alanyl aminopeptidase protein (ANPEP), the meprin A, beta
 CC protein (MEPIB), the aminopeptidase P-like protein (XPN-PEPL), the tissue
 CC kallikrein protein (KLK1), the membrane bound aminopeptidase P protein
 CC (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein
 CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
 CC including the alleles, reference alleles and alternate alleles of the
 CC single nucleotide polymorphisms, listed in the specification. The
 CC polymorphic position resides in a (non) coding position within the genomic
 CC sequence of the gene. The polymorphic position residing in a coding
 CC position results in a missense or silent mutation of the translated
 CC product of the gene. The polymorphic position residing in a non-coding
 CC position resides within the untranslated region or an intronic region of
 CC the gene. Constructing haplotypes using the nucleic acids above further
 CC comprises using the haplotypes to identify an individual for the presence
 CC of a disease phenotype, and correlating the presence of the disease
 CC phenotype with the haplotype. The disease phenotype is angioedema or an
 CC angioedema-like disorder. The nucleic acids, primers and probes are
 CC useful in phenotype correlations, paternity testing, medicine and genetic
 CC analysis. The nucleic acids and polypeptides can be used in diagnosing,
 CC preventing or treating cardiovascular diseases, e.g. angioedema, angina
 CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
 CC stroke, embolism, thrombosis, coronary artery disease or
 CC arteriosclerosis, hypersensitivity reactions during haemodialysis,
 CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
 CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The
 CC present sequence represents a human single nucleotide polymorphism (SNP)
 CC of the invention.

XX Sequence 41 BP; 9 A; 5 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 64.0%; Score 16; DB 12; Length 41;

Best Local Similarity 58.3%; Pred. NO. 1.1e+03;

Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACUUCAGCAUAUUGCCC 25

Db ||:|||||:|||||

34 AACTACAGGATTACACATCTGTC 11

RESULT 5

ADR79899/c

ID ADR79899 standard; DNA; 19 BP.

XX ADR79899;
 CC 16-DEC-2004 (first entry)
 CC Human apolipoprotein B (ApoB) oligonucleotide seqid 4395.
 CC
 CC antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 CC cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
 CC RNA interference; iRNA; antisense technology; lipid metabolism;
 CC cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 CC coronary artery disease; CAD; coronary heart disease; CHD;
 CC atherosclerosis; hepatic glucose production;
 CC glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 CC colon cancer; lung cancer; neurological disease; Huntington disease;
 CC spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
 CC
 CC Homo sapiens.
 CC
 CC WO2004080406-A2.
 CC
 CC 23-SEP-2004.
 CC
 CC 08-MAR-2004; 2004WO-US007070.
 CC
 CC 07-MAR-2003; 2003US-0452682P.
 CC 12-MAR-2003; 2003US-0454265P.
 CC 13-MAR-2003; 2003US-0454962P.
 CC 13-MAR-2003; 2003US-0455050P.
 CC 14-APR-2003; 2003US-0462894P.
 CC 17-APR-2003; 2003US-0463772P.
 CC 25-APR-2003; 2003US-0465665P.
 CC 25-APR-2003; 2003US-0465802P.
 CC 03-MAY-2003; 2003US-0469612P.
 CC 08-AUG-2003; 2003US-0493986P.
 CC 11-AUG-2003; 2003US-0494597P.
 CC 26-SEP-2003; 2003US-0506341P.
 CC 09-OCT-2003; 2003US-0510246P.
 CC 10-OCT-2003; 2003US-0510318P.
 CC 07-NOV-2003; 2003US-0518453P.
 CC
 CC (ALNY-) ALNYLAM PHARM.
 CC
 CC Manoharan M, Bumcrot D;
 CC WPI; 2004-677362/66.
 CC
 CC Interference RNA agent useful for treating dyslipidemias, coronary artery
 CC disease, diabetes, cancer or neurological disease, comprises sense
 CC sequence and antisense sequence which has specific modifications.
 CC
 CC Example 5; SEQ ID NO 4395; 378pp; English.
 CC
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are a pharmaceutical preparation comprising (I); reducing (MI) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (MI)
 CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart

CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
 CC inhibit hepatic glucose production or for treating glucose-metabolism-
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
 CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
 CC can be used to control ApoB gene expression.
 CC
 CC Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
 CC
 CC Query Match 63.2%; Score 15.8; DB 13; Length 19;
 CC Best Local Similarity 57.9%; Pred. No. 1.2e+03;
 CC Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 3 ACUCAGGAUCCAGAUU 21
 CC ||:||| |:|||||:
 CC Db 19 ACTTCAAGGTTCCAGATAT 1
 CC
 CC RESULT 6
 CC ADR77241/C
 CC ID ADR77241 standard; DNA; 19 BP.
 CC XX
 CC AC ADR77241;
 CC XX
 CC DT 16-DEC-2004 (first entry)
 CC XX
 CC DE Human apolipoprotein B (ApoB) oligonucleotide seqid 1726.
 CC XX
 CC KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 CC cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
 CC RNA interference; iRNA; antisense technology; lipid metabolism;
 CC cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 CC coronary artery disease; CAD; coronary heart disease; CHD;
 CC atherosclerosis; hepatic glucose production;
 CC glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 CC colon cancer; lung cancer; neurological disease; Huntington disease;
 CC spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
 CC
 CC Homo sapiens.
 CC
 CC WO2004080406-A2.
 CC
 CC 23-SEP-2004.
 CC
 CC 08-MAR-2004; 2004WO-US007070.
 CC
 CC 07-MAR-2003; 2003US-0452682P.
 CC 12-MAR-2003; 2003US-0454265P.
 CC 13-MAR-2003; 2003US-0454962P.
 CC 13-MAR-2003; 2003US-0455050P.
 CC 14-APR-2003; 2003US-0462894P.
 CC 17-APR-2003; 2003US-0463772P.
 CC 25-APR-2003; 2003US-0465665P.
 CC 25-APR-2003; 2003US-0465802P.
 CC 03-MAY-2003; 2003US-0469612P.
 CC 08-AUG-2003; 2003US-0493986P.
 CC 11-AUG-2003; 2003US-0494597P.
 CC 26-SEP-2003; 2003US-0506341P.
 CC 09-OCT-2003; 2003US-0510246P.
 CC 10-OCT-2003; 2003US-0510318P.
 CC 07-NOV-2003; 2003US-0518453P.
 CC
 CC (ALNY-) ALNYLAM PHARM.
 CC
 CC Manoharan M, Bumcrot D;
 CC WPI; 2004-677362/66.
 CC
 CC Interference RNA agent useful for treating dyslipidemias, coronary artery
 CC disease, diabetes, cancer or neurological disease, comprises sense
 CC sequence and antisense sequence which has specific modifications.
 CC
 CC Example 5; SEQ ID NO 4395; 378pp; English.
 CC
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are a pharmaceutical preparation comprising (I); reducing (MI) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (MI)
 CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart

XX	Example 5; SEQ ID NO 1726; 378pp; English.	
XX	The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2'-O alkyl modifications, the antisense sequences have one or more asymmetrical phosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100 levels or glucose-6-phosphatase levels in a subject; producing (I); stabilising (I), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1) is useful for reducing apob-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apob-100, elevated or otherwise unwanted levels of cholesterol, and/or dysregulation of lipid metabolism. The disorder is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholesterolaemia, statin-resistant disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g. AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.	
XX	Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;	
XX	Query Match 63.2%; Score 15.8; DB 13; Length 19;	
XX	Best Local Similarity 57.9%; Pred. No. 1.2e+03;	
XX	Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;	
QY	3 ACUCAGGAUUCACAGAU 21	
DB	19 ACTTCAGGTTCCAGATAT 1	
XX	RESULT 7	
ID	ADR80185/c	
XX	ADR80185 standard; DNA; 19 BP.	
XX	AC ADR80185;	
XX	16-DEC-2004 (first entry)	
DE	Human apolipoprotein B (ApoB) oligonucleotide seqid 4682.	
XX	antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;	
XX	cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;	
KW	RNA interference; iRNA; antisense technology; lipid metabolism;	
KW	cholesterol imbalance; dyslipidaemia hypercholesterolaemia;	
KW	coronary artery disease; CAD; coronary heart disease; CHD;	
KW	atherosclerosis; hepatic glucose production;	
KW	glucose-metabolism-related disorder; diabetes; cancer; breast cancer;	
KW	colon cancer; lung cancer; neurological disease; Huntington disease;	
KW	spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apob; ss.	
OS	Homo sapiens.	
XX	WO2004080406-A2.	
XX	23-SEP-2004.	
XX	08-MAR-2004; 2004WO-US007070.	
XX	07-MAR-2003; 2003US-0452682P.	
PR	12-MAR-2003; 2003US-045265P.	
XX	13-MAR-2003; 2003US-0454962P.	
XX	13-MAR-2003; 2003US-0455050P.	
XX	14-APR-2003; 2003US-0462894P.	
XX	17-APR-2003; 2003US-0463772P.	
XX	25-APR-2003; 2003US-0465665P.	
XX	25-APR-2003; 2003US-0465802P.	
XX	09-MAY-2003; 2003US-0469612P.	
XX	08-AUG-2003; 2003US-0493986P.	
XX	11-AUG-2003; 2003US-0494597P.	
XX	26-SEP-2003; 2003US-0506341P.	
XX	09-OCT-2003; 2003US-0510246P.	
XX	10-OCT-2003; 2003US-0510318P.	
XX	07-NOV-2003; 2003US-0518453P.	
XX	(ALNY-) ALNYLAM PHARM.	
PI	Manoharan M, Bumcrot D;	
XX	WPI; 2004-677362/66.	
XX	Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.	
PT	Example 5; SEQ ID NO 4682; 378pp; English.	
PS	The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2'-O alkyl modifications, the antisense sequences have one or more asymmetrical phosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100 levels or glucose-6-phosphatase levels in a subject; producing (I); stabilising (I), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1) is useful for reducing apob-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apob-100, elevated or otherwise unwanted levels of cholesterol, and/or dysregulation of lipid metabolism. The disorder is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholesterolaemia, statin-resistant disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g. AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.	
XX	Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;	
XX	Query Match 63.2%; Score 15.8; DB 13; Length 19;	
XX	Best Local Similarity 57.9%; Pred. No. 1.2e+03;	
XX	Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;	
QY	3 ACUCAGGAUUCACAGAU 21	
DB	19 ACTTCAGGTTCCAGATAT 1	
XX	RESULT 8	
ID	ADR76955/c	
XX	ADR76955 standard; DNA; 19 BP.	
XX	AC ADR76955;	
XX	16-DEC-2004 (first entry)	
XX	Query Match 63.2%; Score 15.8; DB 13; Length 19;	
XX	Best Local Similarity 57.9%; Pred. No. 1.2e+03;	
XX	Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;	
QY	3 ACUCAGGAUUCACAGAU 21	
DB	19 ACTTCAGGTTCCAGATAT 1	
XX	RESULT 8	
ID	ADR76955/c	
XX	ADR76955 standard; DNA; 19 BP.	
XX	AC ADR76955;	
XX	16-DEC-2004 (first entry)	

XX Human apolipoprotein B (ApoB) oligonucleotide seqid 1440.
DE antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
XX cytosatic; anticonvulsant; nootropic; muscular; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
OS Homo sapiens.
XX
XX WO2004080406-A2.
XX
XX 23-SEP-2004.
XX
XX 08-MAR-2004; 2004WO-US007070.
XX
XX 07-MAR-2003; 2003US-0452682P.
PR 12-MAR-2003; 2003US-0454265P.
PR 13-MAR-2003; 2003US-0454962P.
PR 13-MAR-2003; 2003US-0455050P.
PR 14-APR-2003; 2003US-0462894P.
PR 17-APR-2003; 2003US-0463772P.
PR 25-APR-2003; 2003US-0465665P.
PR 25-APR-2003; 2003US-0465802P.
PR 09-MAY-2003; 2003US-0469612P.
PR 08-AUG-2003; 2003US-0493986P.
PR 11-AUG-2003; 2003US-0494597P.
PR 26-SEP-2003; 2003US-0506341P.
PR 09-OCT-2003; 2003US-0510246P.
PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX
XX (ALNY-) ALNYLAM PHARM.
XX
XX Manoharan M, Bumcrot D;
XX WPI; 2004-677362/66.
XX
XX Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.
XX
XX Example 5; SEQ ID NO 1440; 378pp; English.
XX
XX The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its
CC activity; a kit comprising (I) and instructions for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidemias, hypercholesterolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or

CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC can be used to control ApoB gene expression.
XX
SQ Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 63.2%; Score 15.8; DB 13; Length 19;
Best Local Similarity 57.9%; Pred. No. 1.2e+03;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 3 ACUUCAGGAUUCAGAUU 21
Db 19 ACTTCAAGGTTCCAGATAT 1
RESULT 9
AAD48330
ID AAD48330 standard; DNA; 20 BP.
XX
XX AAD48330;
XX
XX 24-FEB-2003 (first entry)
DE Apo B3500 DNA amplifying reverse PCR primer.
XX
XX Single nucleotide polymorphism; SNP; antisense therapy; viral infection;
KW PCR; primer; ss.
XX
XX Unidentified.
XX
XX EP1247815-A2.
XX
XX 09-OCT-2002.
XX
XX 25-MAR-2002; 2002EP-00388025.
XX
XX 25-MAR-2001; 2001US-0278598P.
XX
XX (EXIQ-) EXIQON AS.
XX
XX Jakobseen MH, Kongsbak L, Pfundheller H;
XX WPI; 2003-042042/04.
XX
XX Chimeric oligonucleotide useful as primer in nucleic acid extension and
PT amplification reactions and as capture probe in single nucleotide
PT polymorphism assays, has non-modified and modified nucleic acid residues.
XX
XX Example 1; Page 9; 12pp; English.
XX
XX The invention relates to chimeric oligonucleotide containing modified and
CC non-modified nucleic acid residues which are useful as primer in nucleic
CC acid extension and amplification reactions and as capture probe in single
CC nucleotide polymorphism (SNP) assays. Multiple primers are used in
CC multiplex PCR. The invention is useful in diagnostic purposes, as probes
CC in the purification, isolation and detection of pathogenic organisms such
CC as virus, bacteria or fungi, as generic tools for purification,
CC isolation, amplification and detection of nucleic acids from groups of
CC related species such as for instance rRNA from gram- positive or gram
CC negative bacteria, fungi, mammalian cells. It is also useful as an
CC aptamer in molecular diagnostic e.g. in RNA mediated catalytic processes,
CC in specific binding of antibiotics, drugs, amino acids, peptides,
CC structural proteins, protein receptors, saccharides, enzymes,
CC polysaccharides, biological cofactors, nucleic acids, or triphosphates or
CC in the separation of enantiomers from racemic mixtures by stereospecific
CC binding. It is also used in antisense therapy for treating diseases e.g.
CC viral infection. The present sequence is a PCR primer used for amplifying
CC Apo B3500 DNA. This sequence is used in the exemplification of the
XX invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

```

Query Match      63.2%; Score 15.8; DB 10; Length 20;
Best Local Similarity 57.9%; Pred. No. 1.2e+03;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACUCAGGAUCCAGAUU 21
   ||:| | | | | | | | | |
Db 1 ACTTCAAGGTTCCAGAT 19

RESULT 10
AAQ10823/c
ID AAQ10823 standard; DNA; 34 BP.
XX
AC AAQ10823;
XX
DT 09-MAY-1991 (first entry)
DE Pneumocystis carinii 18S rRNA-targeted probe, 1485.
XX
KW Hybridisation assay; pneumonia; AIDS; ss.
XX
OS Synthetic.
XX
PN WO9102092-A.
XX
PD 21-FEB-1991.
XX
PF 11-AUG-1989; 89US-00392679.
XX
PR 11-AUG-1989; 89US-00392679.
XX
PA (GENE-) GENE-TRAK SYST.
XX
PI Shah JS, Buharin A, Lane DJ;
XX
DR WPI; 1991-073563/10.
XX
PT Nucleic acid fragment - capable of hybridising to r RNA or r DNA of
PT pneumocystis carinii, useful as probes for detection of P carinii.
XX
PS Disclosure; Page 11; 36pp; English.
XX
CC This oligonucleotide has a sequence specific for a region of the rDNA of
CC Pneumocystis carinii, the causative agent of pneumonia. It can be used as
CC a probe in hybridisation assays to detect P. carinii in clinical samples.
CC This probe detects human but not most non-human P. carinii isolates. See
CC also AAQ10820-22 and AAQ10824-33
XX
SQ Sequence 34 BP; 12 A; 7 C; 11 G; 4 T; 0 U; 0 Other;

Query Match      62.4%; Score 15.6; DB 2; Length 34;
Best Local Similarity 54.5%; Pred. No. 1.6e+03;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUUCCCC 25
   ||:| | | | | | | | | |
Db 26 CTCTCGATTACCGGTATGCC 5

RESULT 11
AAT42447/c
ID AAT42447 standard; DNA; 34 BP.
XX
AC AAT42447;
XX
DT 25-MAR-2003 (revised)
DT 08-JAN-1997 (first entry)
DE Probe 1485 for P. carinii 18S rRNA.
XX
KW Probe; pneumocystis carinii; 18S rRNA; human; mammal; immunodeficiency;
KW pneumonia; ferret; rat; ss.
XX

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OS Synthetic.
XX
PN US5519127-A.
XX
PD 21-MAY-1996.
XX
PF 21-JAN-1992; 92US-00826657.
XX
PR 11-AUG-1989; 89US-00392679.
XX
PA (STAD ) AMOCO CORP.
XX
PI Lane DJ, Buharin A, Shah J;
XX
DR WPI; 1996-259122/26.
XX
PT Nucleic acid probes specific for human Pneumocystis carinii - provide
PT sensitive, accurate and rapid diagnosis of infection.
XX
PS Claim 1; Col 13-14; 15pp; English.
XX
CC AAT42443-742456 represent probes for human Pneumocystis carinii (Pc) 18S
CC rRNA. Pc infects humans and most mammalian hosts, but rarely cause
CC illness in normal individuals. However, in certain conditions of
CC immunodeficiency, Pc does give rise to life threatening pneumonia. This
CC sequence hybridises to the 18S rRNA at positions 641-652, and is capable
CC of hybridisation to human Pc. These probes can be used as a probe set for
CC a Pc assay. The 1485 (this sequence), 1487 (see AAT42452) and 1159 (see
CC AAT42448) probes are reactive with all human Pc isolates. The probes 1485
CC and 1487 hybridise to rRNA and rDNA of human Pc, but not to other fungi
CC or bacteria. The 1485 and 1487 probes can therefore be used to detect Pc
CC in clinical samples. The rest of these probe sequences are reactive
CC mainly with ferret Pc and non-human strains of Pc. By using these probe
CC sequences, a more sensitive, accurate and rapid diagnosis can be
CC performed, with reduced expense, in comparison to current technology.
CC rRNA is present in the cell at high concentration, and is not likely to
CC undergo lateral transfer. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 34 BP; 12 A; 7 C; 11 G; 4 T; 0 U; 0 Other;

Query Match      62.4%; Score 15.6; DB 2; Length 34;
Best Local Similarity 54.5%; Pred. No. 1.6e+03;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUUCCCC 25
   ||:| | | | | | | | | |
Db 26 CTCTCGATTACCGGTATGCC 5

RESULT 12
ABL40079/c
ID ABL40079 standard; DNA; 41 BP.
XX
AC ABL40079;
XX
DT 15-MAY-2002 (first entry)
DE Phosphoenolpyruvate-dependent sugar phosphotransferase 12 probe 2.
XX
KW Human; phosphoenolpyruvate-dependent sugar phosphotransferase 12; enzyme;
KW cytosolic; haemostatic; virucide; immunomodulatory; haemopathy;
KW antiinflammatory; gene therapy; malignant tumour; HIV infection;
KW human immunodeficiency virus infection; immunological disease;
KW inflammation; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200200830-A2.
XX
PD 03-JAN-2002.
XX
PF 11-JUN-2001; 2001WO-CN000950.
XX

```

```
PR 14-JUN-2000; 2000CN-00116500.
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX WPI; 2002-075674/10.
XX
XX Phosphoenolpyruvate-dependent sugar phosphotransferase 12 and encoding
XX polynucleotide, used in diagnosis and treatment of malignant tumors,
XX hemopathy, human immunodeficiency virus infection, immunological diseases
XX and inflammation.
XX
XX Example 6; Page 16; 33pp; Chinese.
XX
XX The present invention describes human phosphoenolpyruvate-dependent sugar
XX phosphotransferase 12 (I). (I) has cytosolic, haemostatic, virucide,
XX immunomodulatory and antiinflammatory activities. The polynucleotide (II)
XX encoding (I) can be used in gene therapy. (I) and (II) can be used in the
XX diagnosis and treatment of malignant tumour, haemopathy, human
XX immunodeficiency virus (HIV) infection, immunological diseases and
XX various inflammations. The present sequence represents a probe for (I),
XX which is used in an example from the present invention
XX
XX Sequence 41 BP; 8 A; 11 C; 14 G; 8 T; 0 U; 0 Other;
SQ
Query Match 62.4%; Score 15.6; DB 6; Length 41;
Best Local Similarity 59.1%; Pred. No. 1.7e+03;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 4 CUUCAGGAUUCAGAUUGCC 25
DB 39 CTTCCGGATTCAAGCGATGCC 18
RESULT 13
ABL54676/C
ID ABL54676 standard; DNA; 20 BP.
XX
XX ABL54676;
XX
XX 06-JUN-2002 (first entry)
XX
XX Cricetulus griseus dioxin receptor PCR primer SEQ ID NO 6.
XX
XX Cricetulus griseus; dioxin; receptor; PCR; primer; ss.
XX
XX Cricetulus griseus.
XX
XX JP2002045188-A.
XX
XX 12-FEB-2002.
XX
XX 04-AUG-2000; 2000JP-00236762.
XX
XX 04-AUG-2000; 2000JP-00236762.
XX
XX (SUMO) SUMITOMO CHEM CO LTD.
XX
XX WPI; 2002-263573/31.
XX
XX A dioxin receptor gene useful for measuring dioxin-like substances.
XX
XX Example 1; Page 19; 20pp; Japanese.
XX
XX The invention relates to a Cricetulus griseus dioxin receptor gene
XX (ABL54672) encoding a dioxin receptor (ABB08868) or having an amino acid
XX sequence at least 95 % homologous. The dioxin receptor gene can be used
XX for measuring dioxin-like substances. The present sequence is that of a
XX PCR primer, useful to the invention
XX
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 61.6%; Score 15.4; DB 6; Length 20;
Best Local Similarity 70.6%; Pred. No. 1.9e+03;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAUUCAGGAUUCAG 17
DB 17 CAACTTCAGGATTCGG 1
RESULT 14
ABK00567/C
ID ABK00567 standard; RNA; 17 BP.
XX
XX ABK00567;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human NGO Hammerhead Ribozyme #567.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
XX cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
XX muscular; CD20; neurite growth inhibitor gene; NIGO; hammerhead ribozyme;
XX DNazyme; inozyme; G-cleaver; ambersyme; zinzyme; lymphoma; leukaemia;
XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
XX MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
XX inflammatory arthropathy; central nervous system injury;
XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
XX Parkinson's disease; ataxia; Huntington's disease;
XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX
XX 28-FEB-2000; 2000US-0185516P.
XX
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (BLAT/) BLATT L.
XX
XX (MCSW/) MCSWIGGEN J.
XX
XX (CHOW/) CHOWRIIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX Claim 88; Page 75; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NGO). The
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
XX an ambersyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
XX with a YGV motif). The CD20-targetting nucleic acid is used to cleave RNA
XX of CD20 in the presence of a divalent cation that is preferably Mg2+.
XX Furthermore, it may be contacted with a call to reduce CD20 activity of
XX the cell and treat a patient having a condition associated with the level
XX of CD20. The treatment may further comprise the use of one or more
```


FI BRACE H, NEWRYGEN U, CHOWILLA BM,

Search completed: July 30, 2005, 15:45:02
Job time : 309.77 secs

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source
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/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-471A05-019883"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 54.4%; Score 13.6; DB 9; Length 53;
Best Local Similarity 55.0%; Pred. No. 1.5e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACUACAGGAUCCAGAUU 21
||: ||||: ||||: ||:
Db 50 AGCTTGAGGATCCACATAT 31

RESULT 9
AW156165/c
LOCUS
DEFINITION
ae20d03.v1 Gm-cl015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl015-1758 5', mRNA sequence.
ACCESSION
AW156165
VERSION
AW156165.1 GI:6227566
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 55)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert length: 241 Std Error: 0.00
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .55
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl015-1758"
/tissue_type="Mature flowers, field grown plants"
/lab_host="XLI0-Gold"
/clone_lib="Gm-cl015"
/notes="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:

XhoI; This cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR cDNA library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(AT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XLI0-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelding."

ORIGIN
Query Match 54.4%; Score 13.6; DB 2; Length 55;
Best Local Similarity 55.0%; Pred. No. 1.5e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 ACUUCAGGAUCCAGAUUG 22
||: ||||: ||||: ||:
Db 22 ACATTAGGTTCCAGATCTG 3

RESULT 10
BX532084/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-487A04-019572,
genomic survey sequence.
ACCESSION
BX532084
VERSION
BX532084.1 GI:31409214
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsae.
REFERENCE
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
22755829
12874060
REFERENCE
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
REFERENCE
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 59)
Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At5g05120.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
```


was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 53.6%; Score 13.4; DB 1; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 5 UUCAGGAUCCAGAU 19

Db 21 TTCGAGTACAGAT 7

RESULT 13

AJ658580

LOCUS

DEFINITION AJ658580 KN277 Sus scrofa cDNA clone C0005213_H23, mRNA sequence. EST 28-JUN-2004

ACCESSION

AJ658580

VERSION

AJ658580.1

KEYWORDS

EST.

SOURCE

Sus scrofa

ORGANISM

Sus scrofa

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 29)

Anderson, S.I., Finlayson, H.A. and Archibald, A.L.

Development of cDNA and EST resources for studying reproduction and

embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson, S.I.

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred

v0.020425.c. Vector identified by cross match with the -minscore 20

and -mismatch 12 options. Vector: pBluescriptII(SK+) R. Site1: EcoRI

R. Site2: NotI 5' Seq Primer M13f Normalised library constructed

from pooled early embryos, from 8- cell stage to blastocysts.

Clones available from UK Centre for Functional Genomics in Farm

Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,

www.arkgenomics.org.

FEATURES

Location/Qualifiers

1..29

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="C0005213_H23"

/tissue_type="embryo"

/clone_lib="KN277"

/notes="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2:

NotI; Single pass sequencing. Normalised library

constructed from pooled early embryos, from 8-cell stage

to blastocysts."

ORIGIN

source

Query Match 53.6%; Score 13.4; DB 1; Length 29;

Best Local Similarity 60.9%; Pred. No. 1.6e+05;

Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 ACUUCAGGAUCCAGAUAGCCC 25

Db 2 AGTTAAGGAGGCCAGAAATGACC 24

RESULT 14

CR110498/c

LOCUS CR110498 51 bp DNA linear GSS 05-JUL-2004
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN410j21, genomic survey sequence.

ACCESSION CR110498

VERSION CR110498.1

KEYWORDS GSS; genome survey sequence; MICER.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 51)

Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,

Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,

Rogers, J., and Bradley, A.

Direct Submission

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES

Location/Qualifiers

1..51

/organism="Mus musculus"

/mol_type="genomic DNA"

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/clone_lib="MHPN"

ORIGIN

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Best Local Similarity 56.5%; Pred. No. 1.8e+05;

Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGC 23

Db 51 CAATTGAGGAAGCAGATATGC 29

RESULT 15

BM360861

LOCUS

DEFINITION 8 cDNA subtractive library of human rectum adenocarcinoma Homo

sapiens cDNA, mRNA sequence.

ACCESSION BM360861

VERSION BM360861.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 60)

Chen, Y. and Zhang, Y.Z.

Expressed sequence tags from a subtracted cDNA library of human

rectum adenocarcinoma

U.S. Chin. J. Lymphology Oncol. 2 (2), 9-14 (2002)

Contact: Yao Chen

Life Science College of Sichuan University and the department of

anatomy of basic and legal medical institute of west china medical

center of Sichuan University

Chengdu, Sichuan, P.O.Box 610041, P.R.CHINA

Tel: 86 028 5501361

Email: xmxh263.net

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FEATURES

Location/Qualifiers

1..60

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/map="17"

/tissue_type="rectum"

/dev_stage="73 years old"

/clone_lib="cDNA subtractive library of human rectum

adenocarcinoma"

/note="Vector: pMD18T-vector"

ORIGIN

source

Query Match 53.6%; Score 13.4; DB 4; Length 60;
Best Local Similarity 52.2%; Pred. No. 1.9e+05;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCAGAUAGCC 24
|||:|||||:|:|
Db 22 AACCTCAGGATTCTCCCTCTGCC 44

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Job time : 2439.72 secs

Result No.	Score	Query Match	Length	DB	ID	Description
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2	15.6	62.4	33	6	5519127-36	Patent No. 5519127
3	15.6	62.4	33	6	5519127-17	Patent No. 5519127
4	15.6	62.4	33	6	5519127-36	Patent No. 5519127
C 5	15.6	62.4	34	6	5519127-4	Patent No. 5519127
C 6	15.6	62.4	34	6	5519127-4	Patent No. 5519127
7	15.6	62.4	39	6	5519127-33	Patent No. 5519127
8	15.6	62.4	39	6	5519127-33	Patent No. 5519127
9	15	60.0	25	4	US-09-396-196G-88973	Sequence 88973, A
10	14.8	59.2	38	4	US-08-793-273C-22	Sequence 22, Appl
11	14.8	59.2	38	5	PC-US95-11684-22	Sequence 22, Appl
12	14.2	56.8	25	4	US-09-396-196G-64379	Sequence 64379, A
C 13	14.2	56.8	25	4	US-09-396-196G-118281	Sequence 118281, A
C 14	14	56.0	25	4	US-09-396-196G-83713	Sequence 83713, A
C 15	14	56.0	34	6	5519127-14	Patent No. 5519127
C 16	14	56.0	39	6	5519127-34	Patent No. 5519127
17	14	56.0	39	6	5519127-34	Patent No. 5519127
18	14	56.0	39	6	5519127-34	Patent No. 5519127
C 19	14	56.0	48	3	US-09-367-206-34	Sequence 34, Appl
C 20	13.8	55.2	25	4	US-09-396-196G-15817	Sequence 15817, A
C 21	13.8	55.2	27	4	US-09-396-196G-66465	Sequence 64645, A
C 22	13.8	55.2	27	4	US-09-958-940-7	Sequence 7, Appl
C 23	13.8	55.2	36	1	US-08-105-483-64	Sequence 64, Appl
24	13.8	55.2	36	1	US-08-709-209-64	Sequence 64, Appl
25	13.8	55.2	36	1	US-08-458-101-64	Sequence 64, Appl
26	13.8	55.2	59	3	US-09-101-751A-82	Sequence 82, Appl
C 27	13.6	54.4	25	4	US-09-827-998-1853	Sequence 1853, A


```
5519127-33
; LENGTH: 39
Query Match 62.4%; Score 15.6; DB 6; Length 39;
Best Local Similarity 81.8%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUAGCCC 25
DB 10 CUUCAGGAUCCAGAUAGCCC 31

RESULT 9
US-09-396-196G-88973
; Sequence 88973, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88973
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88973

Query Match 60.0%; Score 15; DB 4; Length 25;
Best Local Similarity 56.5%; Pred. No. 6.4e+02;
Matches 13; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 ACUUCAGGAUCCAGAUAGCCC 25
DB 1 ACTTCGGATTCCATTCATGCCC 23

RESULT 10
US-08-793-273C-22
; Sequence 22, Application US/08793273C
; Patent No. 6482410
; GENERAL INFORMATION:
; APPLICANT: Crossin, Kathryn L.
; APPLICANT: Phillips, Greg
; APPLICANT: Prieto, Anne L.
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND
; TITLE OF INVENTION: NEURITE OUTGROWTH, AND METHODS OF MAKING SAME
; FILE REFERENCE: BEC0022S
; CURRENT APPLICATION NUMBER: US/08/793,273C
; CURRENT FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: PCT/US95/11684
; PRIOR FILING DATE: 1995-09-14
; PRIOR APPLICATION NUMBER: 08/308,359
; PRIOR FILING DATE: 1994-09-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-793-273C-22

Query Match 59.2%; Score 14.8; DB 4; Length 38;
Best Local Similarity 61.1%; Pred. No. 8.6e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 UUCAGGAUCCAGAUAG 22
DB 14 TTCAGAAATTCAGAAATG 31

RESULT 11
PCT-US95-11684-22
; Sequence 22, Application PC/TUS9511684
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
; TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11684
; FILING DATE: 14-SEP-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,359
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: BEC0019P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-11684-22

Query Match 59.2%; Score 14.8; DB 5; Length 38;
Best Local Similarity 61.1%; Pred. No. 8.6e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 UUCAGGAUCCAGAUAG 22
DB 14 TTCAGAAATTCAGAAATG 31

RESULT 12
US-09-396-196G-64379
; Sequence 64379, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
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; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-64379

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Best Local Similarity 57.9%; Pred. No. 1.6e+03;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUAG 22
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RESULT 13
US-09-396-196G-118281/c
; Sequence 118281, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118281
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-118281

Query Match      56.8%; Score 14.2; DB 4; Length 25;
Best Local Similarity 63.2%; Pred. No. 1.6e+03;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUAG 22
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Db 24 CTCAGGACTCCAGGAATG 6

RESULT 14
US-09-396-196G-83713/c
; Sequence 83713, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83713
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
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US-09-396-196G-83713

Query Match      56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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Db 22 CATCTTCAAGTTCTCTGATGTG 1

RESULT 15
5519127-14/c
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA,BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:14
; LENGTH: 34
5519127-14

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Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUAGCCC 25
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Db 26 CTTCTGGATTACCAATATGCTC 5

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Job time : 87.8378 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-544-776-5

Perfect score: 24
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Scoring table: IDENTITY NUC
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1981570

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	17	70.8	17	6	AX216092 Sequence
C 3	17	70.8	17	6	AX216332 Sequence
C 4	17	70.8	17	6	AX216639 Sequence
C 5	17	70.8	17	6	AX217251 Sequence
C 6	16	66.7	17	6	AX216090 Sequence
C 7	16	66.7	17	6	AX217252 Sequence
8	15.6	65.0	60	9	AF200461 Homo sapi
9	15.4	64.2	60	6	CQ537206 Sequence
10	15.2	63.3	51	6	CQ001884 Sequence
C 11	15	62.5	17	6	AX215272 Sequence
C 12	15	62.5	17	6	AX216640 Sequence
13	14.6	60.8	32	6	AR217875 Sequence
14	14.4	60.0	60	6	CQ550946 Sequence
15	14.2	59.2	23	6	CQ809740 Sequence
16	14.2	59.2	24	6	AR069203 Sequence
17	14.2	59.2	24	6	I64421 Sequence 43
18	14.2	59.2	24	6	AX444667 Sequence
19	14.2	59.2	32	6	E49827 apoptosis-1

20	14.2	59.2	32	6	BD094992	BD094992 Apoptosis
21	14	58.3	33	6	AX317512	AX317512 Sequence
C 22	14	58.3	33	6	AX317513	AX317513 Sequence
23	14	58.3	46	6	AI17061	AI17061 oligonucleo
24	14	58.3	46	6	I11879	I11879 Sequence 45
C 25	14	58.3	60	6	CQ536100	CQ536100 Sequence
26	14	58.3	60	6	CQ538479	CQ538479 Sequence
C 27	13.8	57.5	20	6	AR075704	AR075704 Sequence
C 28	13.8	57.5	20	6	I85582	I85582 Sequence 3
29	13.8	57.5	20	6	AR307896	AR307896 Sequence
C 30	13.8	57.5	22	6	AX497015	AX497015 Sequence
C 31	13.8	57.5	23	6	BD259944	BD259944 LIM miner
C 32	13.8	57.5	23	6	AR227706	AR227706 Sequence
C 33	13.8	57.5	23	6	AR282708	AR282708 Sequence
C 34	13.8	57.5	23	6	AR369800	AR369800 Sequence
C 35	13.8	57.5	23	6	BD073527	BD073527 Novel bon
C 36	13.8	57.5	33	6	AR369001	AR369001 Sequence
C 37	13.8	57.5	33	6	BD011033	BD011033 HIV probe
38	13.6	56.7	25	6	A47542	A47542 Sequence 37
39	13.6	56.7	25	6	AR097953	AR097953 Sequence
40	13.6	56.7	25	6	AX116788	AX116788 Sequence
41	13.6	56.7	30	6	BD168952	BD168952 Drug resi
42	13.6	56.7	30	6	I13289	I13289 Sequence 9
C 43	13.6	56.7	51	6	AX116789	AX116789 Sequence
C 44	13.6	56.7	60	6	CQ547591	CQ547591 Sequence
C 45	13.6	56.7	60	6	CQ548554	CQ548554 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX216091 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1533 from Patent WO0159103.
ACCESSION AX216091
VERSION AX216091.1 GI:15526134
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B. M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1533 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source location/Qualifiers
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Best Local Similarity 82.4%; Pred. No. 1e+04;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 UCCACCAGGCCUCAGA 19
Db 17 TCCACCAGTGCCTCAGA 1
RESULT 2
AX216092/c
LOCUS AX216092 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1534 from Patent WO0159103.
ACCESSION AX216092
VERSION AX216092.1 GI:15526135
KEYWORDS synthetic construct
SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1534 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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Best Local Similarity 76.5%; Pred. No. 1e+04;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AUUCCACGAGGCUCA 17
Db 17 ATTCCACGAGTGCCTCA 1
RESULT 3
AX216332/c
LOCUS AX216332 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1774 from Patent W00159103.
ACCESSION AX216332
VERSION AX216332.1 GI:15526393
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1774 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
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Best Local Similarity 82.4%; Pred. No. 1e+04;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 8 CAGUGCCUCAGUAGGA 24
Db 17 CAGTGCTCAGATAGGA 1
RESULT 4
AX216639/c
LOCUS AX216639 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2081 from Patent W00159103.
ACCESSION AX216639
VERSION AX216639.1 GI:15526700
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression
Patent: WO 0159103-A 2081 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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Best Local Similarity 82.4%; Pred. No. 1e+04;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 5 CACCAGUGCCUCAGUAU 21
Db 17 CACCAGTGCCTCAGATA 1
RESULT 5
AX217251/c
LOCUS AX217251 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2693 from Patent W00159103.
ACCESSION AX217251
VERSION AX217251.1 GI:15527312
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2693 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
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/note="Nucleic Acid"
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Best Local Similarity 82.4%; Pred. No. 1e+04;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 6 ACCAGUGCCUCAGUAUAG 22
Db 17 ACCAGTGCCTCAGATAG 1
RESULT 6
AX216090/c
LOCUS AX216090 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1532 from Patent W00159103.
ACCESSION AX216090
VERSION AX216090.1 GI:15526133
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1532 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers


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source
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/note="Nucleic Acid"

ORIGIN
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Best Local Similarity 81.2%; Pred. No. 3.1e+04;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 17 AGTGCTCAGATAGGA 2

RESULT 7
LOCUS AX217252/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2694 from Patent WO0159103.
ACCESSION AX217252
VERSION AX217252.1 GI:15527313
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J., and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 2694 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
LOCATION/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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FEATURES
source
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Best Local Similarity 75.0%; Pred. No. 3.1e+04;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGGCTC 16
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Db 16 ATCCACGAGTGCCTC 1

RESULT 8
LOCUS AF200461 60 bp mRNA linear PRI 01-MAR-2000
DEFINITION Homo sapiens T-cell receptor beta mRNA, partial cds.
ACCESSION AF200461
VERSION AF200461.1 GI:7110211
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 60)
JOURNAL Pachman, L.M., Liotta, M.R., Lawton, T., Morello, P., Pope, R.M.,
Wu, T.T. and Concannon, P.
REFERENCE 2
AUTHORS New Onset Juvenile Dermatomyositis: Evidence of Vbetas T cell
TITLE Receptor Oligoclonality in Muscle Biopsies of DQAI*0501 Caucasian
JOURNAL Children
REFERENCE 2
AUTHORS (bases 1 to 60)
TITLE Pachman, L.M., Liotta, M.R., Lawton, T., Morello, P., Pope, R.M.,
Wu, T.T. and Concannon, P.
JOURNAL Direct Submission
TITLE Submitted (01-NOV-1999) Immunology, Children's Memorial Institute

for Education and Research (CMIER), 2430 N. Halsted, Chicago, IL
60614, USA
FEATURES
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/protein id="AAP36828.1"
/db_xref="GI:7110212"
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Best Local Similarity 63.6%; Pred. No. 3.7e+04;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

ORIGIN
Qy 2 UUCCACGAGGCTCUCAGAUAGG 23
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Db 13 TGCCAGCAGTTCCTCATATAGG 34

RESULT 9
LOCUS CQ537206 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6841 from Patent WO0210449.
ACCESSION CQ537206
VERSION CQ537206.1 GI:41503470
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
JOURNAL Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
PATENT: WO 0210449-A 6841 07-FEB-2002;
Compugen Inc. (US)
LOCATION/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 64.2%; Score 15.4; DB 6; Length 60;
Best Local Similarity 76.5%; Pred. No. 4.6e+04;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ACCGAGGCTCUCAGAUAG 22
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Db 2 ACCAGTGCCTCAGGTAG 18

RESULT 10
LOCUS CQ001884 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 524 from Patent WO0147944.
ACCESSION CQ001884
VERSION CQ001884.1 GI:41008516
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shinketsu, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0147944-A 524 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Accession number cg43948635"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 51;
Best Local Similarity 70.0%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 UCCACGAGGCGCCGAGUAG 22
18 TCCGTCAGTGCCTCAGACAG 37

Db

RESULT 11
AX215272/c
LOCUS AX215272 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 714 from Patent WO0159103.
ACCESSION AX215272
VERSION AX215272.1 GI:15525315
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 714 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

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Best Local Similarity 80.0%; Pred. No. 9.1e+04;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 GUGCCUCAGAUAGGA 24
17 GTGCCTCAGTAGGA 3

Db

RESULT 12
AX216640/c
LOCUS AX216640 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2082 from Patent WO0159103.
ACCESSION AX216640
VERSION AX216640.1 GI:15526701
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 2082 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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/note="Nucleic Acid"

ORIGIN
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Best Local Similarity 73.3%; Pred. No. 9.1e+04;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGGCGCU 15
15 ATTCCACCAGTGCCT 1

Db

RESULT 13
AR217875
LOCUS AR217875 32 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 12 from patent US 6417002.
ACCESSION AR217875
VERSION AR217875.1 GI:23317769
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Horlick, R.A. and Chelsky, D.
TITLE Method for maintenance and selection of episomes
JOURNAL Patent: US 6417002-A 12 09-JUL-2002;
FEATURES
source Location/Qualifiers
1..32
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/mol_type="genomic DNA"

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Best Local Similarity 61.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 UCCACGAGGCGCCGAGUAGG 23
12 TTCACCTTGCGCTCAGTAGG 32

Db

RESULT 14
CQ550946
LOCUS CQ550946 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 20581 from Patent WO0210449.
ACCESSION CQ550946
VERSION CQ550946.1 GI:41517373
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 20581 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source Location/Qualifiers
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Search completed: July 30, 2005, 16:20:41
Job time : 690.514 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:18:17 ; Search time 295.459 Seconds
(without alignments)
480.857 Million cell updates/sec

Title: US-09-544-776-5
Perfect score: 24
Sequence: 1 aauccacagucucagauagga 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4316768

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980a:*
2: Geneseqn1990a:*
3: Geneseqn2000a:*
4: Geneseqn2001a:*
5: Geneseqn2001bs:*
6: Geneseqn2002a:*
7: Geneseqn2002bs:*
8: Geneseqn2003a:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004a:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	3	Aac64409 Human Nog
2	22	91.7	25	12	Adp17627 Renal cel
3	17	70.8	17	4	Abk02693 Human NOG
4	17	70.8	17	4	Abk01533 Human NOG
5	17	70.8	17	4	Abk01534 Human NOG
6	17	70.8	17	4	Abk02081 Human NOG
7	17	70.8	17	4	Abk01774 Human NOG
8	17	70.8	25	12	Adp17626 Renal cel
9	16	66.7	17	4	Abk01532 Human NOG
10	16	66.7	17	4	Abk02694 Human NOG
11	15.6	65.0	22	12	Adp48303 Human lym
12	15.6	65.0	30	2	Aav05323 PCR prime
13	15.4	64.2	20	6	Abk68889 Human Rec
14	15.4	64.2	60	6	Abn34093 Human SNP
15	15.2	63.3	51	4	Aal27316 Human NOG
16	15	62.5	17	4	Abk02082 Human NOG
17	15	62.5	17	4	Abk00714 Human NOG
18	15	62.5	50	6	Abi00669 Human leu
19	14.6	60.8	25	9	Ac132957 Human mic
20	14.4	60.0	46	3	Aaa29906 Promoter

C	21	14.4	60.0	46	3	AAA29903	Aaa29903 Promoter
C	22	14.4	60.0	50	6	ABZ06526	Abz06526 Human leu
C	23	14.4	60.0	50	6	ABZ06536	Abz06536 Human leu
C	24	14.4	60.0	57	12	ADG99916	Adg99916 Kidney di
C	25	14.4	60.0	60	6	ABN47833	Abn47833 Human spl
C	26	14.2	59.2	23	12	ADO07638	Ado07638 Transgeni
C	27	14.2	59.2	24	2	AAT98136	Aat98136 Primer V-
C	28	14.2	59.2	24	2	AAx85979	Aax85979 PCR prime
C	29	14.2	59.2	24	2	AAx88155	Aax88155 T cell re
C	30	14.2	59.2	24	6	ABQ06198	Abq06198 Oligonuc1
C	31	14.2	59.2	24	6	ABQ06157	Abq06157 Oligonuc1
C	32	14.2	59.2	24	6	ABQ01115	Abq01115 Oligonuc1
C	33	14.2	59.2	25	9	ACI45153	Act45153 Human mic
C	34	14.2	59.2	31	3	AAAS0260	Aaa50260 Bcl2 gene
C	35	14.2	59.2	32	4	AAH45308	Aah45308 Human Bcl
C	36	14	58.3	33	4	AAI66468	Aai66468 P53 tumou
C	37	14	58.3	33	7	ADI92962	Adi92962 Thermus s
C	38	14	58.3	33	7	ADI92963	Adi92963 Thermus s
C	39	14	58.3	47	13	ADR37349	Adr37349 Human nic
C	40	14	58.3	47	13	ADR37347	Adr37347 Human nic
C	41	14	58.3	47	13	ADR37350	Adr37350 Human nic
C	42	14	58.3	47	13	ADR37348	Adr37348 Human nic
C	43	14	58.3	60	6	ABN35366	Abn35366 Human spl
C	44	14	58.3	60	6	ABN32987	Abn32987 Human spl
C	45	13.8	57.5	20	2	AA700607	Aat00607 21-hydrox

ALIGNMENTS

RESULT 1
AAC64409
ID AAC64409 standard; RNA; 24 BP.

XX AAC64409;
XX
XX 08-FEB-2001 (first entry)

XX Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:5.

XX Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
XX stress-phosphorylated endoplasmic reticulum protein; cytosolic;
XX gene therapy; cell growth; cellular stress response; neuron growth;
XX regulator of oxidative stress; inhibitor of neurite outgrowth;
XX axon regeneration; diagnosis; cancer; identification; antisense;
XX phosphorothioate; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH modified_base 1..24
FT FT /*tag= a
FT /note= "phosphorothioate linkages"

XX WO2000060083-A1.

XX 12-OCT-2000.

XX 07-APR-2000; 2000WO-US009383.

XX 08-APR-1999; 99US-0128372P.

XX 21-JUN-1999; 99US-0140331P.

XX (CHIR) CHIRON CORP.

XX Wei D, Halenbeck R, Williams LT;

XX WPI; 2000-665007/64.

XX Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

PS Claim 25; Page 32; 60pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic

CC reticulum protein, designated Nogo B. Nogo B has cytosolic activity and

CC is a modulator of the storage and exchange of calcium, cell growth and

CC cellular stress response. It can: regulate oxidative stress; inhibit

CC neurite outgrowth, neuron growth and axon regeneration. Nogo B

CC polypeptides and polynucleotides are useful for modulating stress levels

CC and cellular stress-response, cell growth and viability, diagnosis and

CC treatment of cancer, malignant growth and other Nogo B related diseases.

CC Nogo B polypeptides are also useful to screen combinatorial libraries to

CC identify agonist or antagonist. Antibodies against Nogo B polypeptides

CC are useful for affinity chromatography and distinguishing Nogo B

CC polypeptides. The present sequence represents a human Nogo B

CC phosphorothioate antisense oligonucleotide from the present invention

XX

SQ Sequence 24 BP; 7 A; 7 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUCAGAUAGGA 24

|||||

Db 1 AUUCCACCAGUGCCUCAGAUAGGA 24

|||||

RESULT 2

ID ADP17627/c

XX ADP17627 standard; DNA; 25 BP.

AC ADP17627;

XX

DT 26-AUG-2004 (first entry)

XX

DE Renal cell carcinoma differentially expressed gene probe #4032.

DE ss; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KW head/neck cancer; differential expression; probe.

XX

OS Homo sapiens.

XX

PN WO2004048933-A2.

XX

PD 10-JUN-2004.

XX

XX 21-NOV-2003; 2003WO-US037481.

PF

XX 21-NOV-2002; 2002US-0427982P.

PR

XX 03-APR-2003; 2003US-0459782P.

XX

(AMHP) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STON/) STOVER J A.

PA (SLON/) SLONI D K.

XX

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

PI WPI; 2004-460799/43.

DR

XX Diagnosing non-blood disease such as solid tumor, involves comparing

PT differential expression profile of specific genes in peripheral blood

PT sample of subject with reference expression profile of specific genes.

XX

PS Disclosure; SEQ ID NO 4363; 350pp; English.

XX

XX The invention relate to a method of diagnosing (M1) non-blood disease

CC such as solid tumor by providing peripheral blood sample of human having

CC

CC non-blood disease, and comparing an expression profile of specific genes

CC in the peripheral blood sample to reference expression profile of the

CC genes, where each of the genes is differentially expressed in peripheral

CC blood mononuclear cells (PBMCs) of patients having the disease as

CC compared to PBMCs of normal humans. The method is useful for diagnosing

CC non-blood disease such as solid tumor. The solid tumor is chosen from

CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The

CC peripheral blood sample comprises enriched PBMCs. The peripheral blood

CC sample is a whole blood sample (claimed). (M1) is useful for identifying

CC genes that are differentially expressed in peripheral blood samples

CC isolated at different stages of progression, development or treatment of

CC RCC and/or other solid tumors. This sequence corresponds to a probe to

CC detect a gene that is differentially expressed and detected by the method

CC of the invention.

XX

SQ Sequence 25 BP; 8 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 91.7%; Score 22; DB 12; Length 25;

Best Local Similarity 77.3%; Pred. No. 1.1;

Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUCAGAUAG 22

|||||

Db 22 ATTCCACCAGTGCCTCAGATAG 1

|||||

RESULT 3

ABK02693/c

ID ABK02693 standard; RNA; 17 BP.

XX

AC ABK02693;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human Nogo Amberzyme #365.

XX

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead ribozyme;

KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200159103-A2.

XX

XX 16-AUG-2001.

PD

XX 09-FEB-2001; 2001WO-US004273.

PF

XX 11-FEB-2000; 2000US-0181797P.

PR

XX 28-FEB-2000; 2000US-0185516P.

PR

XX 06-MAR-2000; 2000US-0187128P.

PR

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX

XX Blatt L, Mcswiggen J, Chowrira BM;

PI

XX WPI; 2001-607195/69.

DR

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT

growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 88; Page 139; 20pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zincyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV human immunodeficiency virus associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an amberzyme molecule of the invention

Sequence 17 BP; 3 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 70.8%; Score 17; DB 4; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.7e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0

QY 6 ACCAGUGCCUCAGAUAG 22
|||||:||||:||||:
Db 17 ACCAGTGCCTCAGATAG 1

RESULT 4
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ID ABK01533 standard; RNA; 17 BP.
AC ABK01533;
XX
XX
XX 12-MAR-2002 (first entry)
XX
XX Human NOGO Inozyme #803.
DE
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
XX cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberzyme; zincyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX Homo sapiens.
OS Synthetic.

ABK01534;
 12-MAR-2002 (first entry)
 Human NOGO Inozyme #804.
 Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 Homo sapiens.
 Synthetic.
 WO200159103-A2.
 16-AUG-2001.
 09-FEB-2001; 2001WO-US004273.
 11-FEB-2000; 2000US-0181797P.
 28-FEB-2000; 2000US-0185516P.
 06-MAR-2000; 2000US-0187128P.
 (RIBO-) RIBOZYME PHARM INC.
 (BLAT/) BLATT L.
 (MCSW/) MCSWIGGEN J.
 (CHOW/) CHOWRIRA B M.
 Blatt L, Mcswiggen J, Chowrira BM;
 WPI; 2001-607195/69.
 Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
 Claim 88; Page 90; 200pp; English.
 The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob CC disease, muscular dystrophy, and/or other neurodegenerative disease CC states which respond to the modulation of NOGO expression. The present CC sequence is an inozyme of the invention
 XX
 SQ Sequence 17 BP; 4 A; 2 C; 7 G; 0 T; 4 U; 0 Other;
 Query Match 70.8%; Score 17; DB 4; Length 17;
 Best Local Similarity 76.5%; Pred. No. 2.7e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AUUCCACCAGUGCCUCA 17
 Db 17 ATTCCACCAGUGCCCTCA 1
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 ABK02081/c
 ID ABK02081 standard; RNA; 17 BP.
 XX
 AC ABK02081;
 XX
 DT 12-MAR-2002 (first entry)
 DE Human NOGO Zinczyme #403.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 Homo sapiens.
 Synthetic.
 WO200159103-A2.
 16-AUG-2001.
 09-FEB-2001; 2001WO-US004273.
 11-FEB-2000; 2000US-0181797P.
 28-FEB-2000; 2000US-0185516P.
 06-MAR-2000; 2000US-0187128P.
 (RIBO-) RIBOZYME PHARM INC.
 (BLAT/) BLATT L.
 (MCSW/) MCSWIGGEN J.
 (CHOW/) CHOWRIRA B M.
 Blatt L, Mcswiggen J, Chowrira BM;
 WPI; 2001-607195/69.
 Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
 Claim 88; Page 102; 200pp; English.
 The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zynzyme molecule of the invention
 XX
 SQ Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;
 Query Match 70.8%; Score 17; DB 4; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.7e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CACGAGUGCTUCAGUA 21
 |||||:||||:||||:
 DB 17 CACGAGTGCCTCAGATA 1
 RESULT 7
 ABK01774/c
 ID ABK01774 standard; RNA; 17 BP.
 AC ABK01774;
 DT 12-MAR-2002 (first entry)
 XX Human NOGO Zynzyme #96.
 KW Human; as; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNAzyme; inozyme; G-cleaver; amberzyme; zynzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 PN 16-AUG-2001.
 PD 09-FEB-2001; 2001WO-US004273.
 XX

PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 XX constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 95; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zynzyme molecule of the invention
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 70.8%; Score 17; DB 4; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.7e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CAGUGCTUCAGUA 24
 |||||:||||:||||:
 DB 17 CAGTGCCTCAGATAGGA 1
 RESULT 8
 ADP17626/c
 ID ADP17626 standard; DNA; 25 BP.
 XX
 AC ADP17626;
 XX
 XX 26-AUG-2004 (first entry)
 DT
 XX Renal cell carcinoma differentially expressed gene probe #4031.
 DE
 XX

KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
 KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
 KW head/neck cancer; differential expression; probe.
 XX
 OS Homo sapiens.
 XX WO2004048933-A2.
 PN 10-JUN-2004.
 PD
 XX 21-NOV-2003; 2003WO-US037481.
 XX 21-NOV-2002; 2002US-0427982P.
 PR 03-APR-2003; 2003US-0459782P.
 XX (AMHP) WYETH.
 PA (TWIN/) TWINE N C.
 PA (BURC/) BURCZYNSKI M E.
 PA (TREP/) TREPICCHIO W L.
 PA (DORN/) DORNER A.
 PA (STOV/) STOVER J A.
 PA (SLON/) SLONI D K.
 XX Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;
 PI Sloni DK;
 XX WPI; 2004-460799/43.
 DR
 XX Diagnosing non-blood disease such as solid tumor, involves comparing
 PT differential expression profile of specific genes in peripheral blood
 PT sample of subject with reference expression profile of specific genes.
 XX
 PS Disclosure; SEQ ID NO 4362; 350pp; English.
 XX
 CC The invention relate to a method of diagnosing (M1) non-blood disease
 CC such as solid tumor by providing peripheral blood sample of human having
 CC non-blood disease, and comparing an expression profile of specific genes
 CC in the peripheral blood sample to reference expression profile of the
 CC genes, where each of the genes is differentially expressed in peripheral
 CC blood mononuclear cells (PBMCs) of patients having the disease as
 CC compared to PBMCs of normal humans. The method is useful for diagnosing
 CC non-blood disease such as solid tumor. The solid tumor is chosen from
 CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
 CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
 CC sample is a whole blood sample (claimed). (M1) is useful for identifying
 CC genes that are differentially expressed in peripheral blood samples
 CC isolated at different stages of progression, development or treatment of
 CC RCC and/or other solid tumors. This sequence corresponds to a probe to
 CC detect a gene that is differentially expressed and detected by the method
 CC of the invention.
 XX
 SQ Sequence 25 BP; 4 A; 6 C; 4 G; 11 T; 0 U; 0 Other;
 Query Match 70.8%; Score 17; DB 12; Length 25;
 Best Local Similarity 82.4%; Pred. No. 2.9e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CAGUGCCUCAGUAGGA 24
 |||:|||||:|||||
 Db 25 CAGTGCCTCAGATAGGA 9
 RESULT 9
 ABK01532/c
 ID ABK01532 standard; RNA; 17 BP.
 XX
 AC ABK01532;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme #802.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 PN 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004273.
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 90; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyze (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX

SQ Sequence 17 BP; 3 A; 5 C; 3 G; 0 T; 6 U; 0 Other;
 Query Match 66.7%; Score 16; DB 4; Length 17;
 Best Local Similarity 81.2%; Pred. No. 8.2e+02;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 9 AGUGCCUCAGUAGCA 24
 ||:||||:||||:||||
 Db 17 AGTGCCCTCAGATAGGA 2

RESULT 10
 ID ABK02694/C
 XX ABK02694 standard; RNA; 17 BP.
 AC ABK02694;
 DT 12-MAR-2002 (first entry)
 XX Human NOGO Amberzyme #366.
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; TMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Homo sapiens.
 OS Synthetic.
 XX WO2000159103-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004273.
 XX 11-FEB-2000; 2000US-0181797P.
 XX 28-FEB-2000; 2000US-0185516P.
 XX 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX Claim 88; Page 139; 200pp; English.
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an amberzyme molecule of the invention
 XX SQ Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 66.7%; Score 16; DB 4; Length 17;
 Best Local Similarity 75.0%; Pred. No. 8.2e+02;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUC 16
 ||:||||:||||:||||
 Db 16 ATTCACCAGTGCCTC 1

RESULT 11

ID ADP48303/C
 XX ADP48303 standard; DNA; 22 BP.

AC ADP48303;
 XX 09-SEP-2004 (first entry)

XX Human lymphocyte specific tyrosine kinase (Lck) DNA PCR primer #2.
 DE Human lymphocyte specific tyrosine kinase; Lck; PCR; ss;
 XX antisense oligonucleotide; phosphorothioate linkage;
 KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
 KW hyperproliferative disorder; cancer; cytostatic; primer.

XX Homo sapiens.
 OS US2004116365-A1.
 XX 17-JUN-2004.
 XX 10-DEC-2002; 2002US-00316515.
 XX 10-DEC-2002; 2002US-00316515.
 XX (ISIS-) ISIS PHARM INC.
 PA Borchers AH, Freier SM;
 PI WPI; 2004-498280/47.
 XX New antisense oligonucleotide compounds, useful for diagnosing,
 PT preventing and/or treating diseases or conditions associated with
 PT aberrant expression or activity of Lck, such as hyperproliferative
 PT disorders.
 XX Claim 21; SEQ ID NO 6; 40pp; English.
 XX The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.

Db 1 CCACGAGTGCCTCAGGT 17

RESULT 14
ABN34093
ID ABN34093 standard; DNA; 60 BP.
XX
AC ABN34093;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6841.
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Paigler S;
XX
XX WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 6841; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 16 A; 10 C; 20 G; 14 T; 0 U; 0 Other;
Query Match 64.2%; Score 15.4; DB 6; Length 60;
Best Local Similarity 76.5%; Pred. No. 1.9e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 6 ACCAGGCGCTCAGGAG 22
|||||:|||||:|
Db 2 ACCAGGCGCTCAGGAG 18

RESULT 15
AAL27316
ID AAL27316 standard; DNA; 51 BP.
XX
AC AAL27316;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #524.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 1539; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 9 A; 16 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 63.3%; Score 15.2; DB 4; Length 51;
Best Local Similarity 70.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 UCCACGAGGCGCTCAGGAG 22
:|||||:|||||:|
Db 18 TCCGTCAGTGCCTCAGAC 37

Search completed: July 30, 2005, 15:45:04

Job time : 297.459 secs

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:01:12 ; Search time 2331.57 Seconds
(without alignments)
391.815 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 auccaccaguccagauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	66.7	31	1	A1768291	A1768291 wg83f08.x
2	14.6	60.8	50	8	A2452836	A2452836 1M0252H23
3	14	58.3	42	8	A2452625	A2452625 1M0252002
C 4	14	58.3	44	8	A2595168	A2595168 1M0407C07
C 5	14	58.3	57	2	BF143628	BF143628 601790985
C 6	13.8	57.5	58	1	A1327266	A1327266 mo05a08.x
C 7	13.6	56.7	33	8	A2588961	A2588961 1M0397C07
C 8	13.4	55.8	30	8	BH851910	BH851910 SALK 0736
C 9	13.4	55.8	31	9	CL903303	CL903303 RRX310 Ba
C 10	13.4	55.8	56	8	B2660828	B2660828 SALK 0242
C 11	13.2	55.0	31	1	A1443458	A1443458 sa33n08.y
C 12	13.2	55.0	41	8	A2604085	A2604085 1M0423G16
C 13	13.2	55.0	52	1	AA782065	AA782065 ai47b09.s
C 14	13.2	55.0	52	9	CL522553	CL522553 SAMGB01.F
C 15	13.2	55.0	53	8	CC178725	CC178725 XA060 Bay
C 16	13.2	55.0	55	5	BQ565211	BQ565211 gi32h06.y
C 17	13	54.2	25	8	A2391820	A2391820 1M0153B23
C 18	13	54.2	28	8	A2366396	A2366396 1M0115C10
C 19	13	54.2	43	1	AA075907	AA075907 zm74e08.r
C 20	13	54.2	46	1	A1463335	A1463335 vw61d08.x
C 21	13	54.2	50	1	AUI02331	AUI02331 AUI02331
C 22	13	54.2	50	1	AUI02334	AUI02334 AUI02334
C 23	13	54.2	50	1	AUI02335	AUI02335 AUI02335
C 24	13	54.2	50	1	AUI02336	AUI02336 AUI02336

25	13	54.2	52	1	AJ742173	AJ742173
26	13	54.2	53	9	CL459396	CL459396 AH0444 Sa
C 27	13	54.2	58	8	BZ287603	BZ287603 SALK_0209
C 28	12.8	53.3	36	1	AV833686	AV833686 AV833686
C 29	12.8	53.3	51	8	AZ314162	AZ314162 1M0030014
C 30	12.8	53.3	53	7	CN849116	CN849116 000818AAF
C 31	12.8	53.3	54	9	AG193022	AG193022 Pan trogl
C 32	12.8	53.3	55	8	BZ767951	BZ767951 SALK_1395
C 33	12.6	52.5	48	9	AL940086	AL940086 Arabidops
C 34	12.6	52.5	50	1	AUI03667	AUI03667 AUI03667
C 35	12.6	52.5	50	1	AUI03674	AUI03674 AUI03674
C 36	12.6	52.5	50	2	AW396348	AW396348 sh27a03.Y
C 37	12.6	52.5	52	7	N29657	N29657 Vw73c07.e1
C 38	12.6	52.5	54	9	CL528462	CL528462 ASV13E10
C 39	12.6	52.5	55	9	TA108F04P	TA108F04P T. brucei
C 40	12.6	52.5	57	1	AL595919	AL595919 AL595919
C 41	12.6	52.5	59	1	AA705635	AA705635 zf40a11.8
C 42	12.4	51.7	30	9	TA179H01P	TA179H01P T. brucei
C 43	12.4	51.7	31	8	AZ365377	AZ365377 1M0112805
C 44	12.4	51.7	34	8	AZ309860	AZ309860 1M0017007
C 45	12.4	51.7	37	8	BZ664151	BZ664151 SALK_0277

ALIGNMENTS

RESULT 1
A1768291
LOCUS
DEFINITION wg83f08.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone IMAGE:2371719 3' similar to TR:060735 060735 GAL7 PROTEIN. ; mRNA sequence.
ACCESSION A1768291
VERSION A1768291.1 GI:5234800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1006 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2371719"
/lab_host="DH10B"
/clone_lib="Soares NSF F8 9W OT PA P S1"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries and cloneIDs: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HF8-3W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NbhOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 66.7%; Score 16; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. No. 9.2e+03;
Matches 16; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCGCUCAGAUAGGA 24
|||:|||||:|||||:|||||:|||||
DB 7 AATCCCAAGTGCCTCATAAGTA 30

RESULT 2

AZ452836 50 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
1M0252H23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0252H23 R, genomic survey sequence.

ACCESSION
AZ452836
VERSION
AZ452836.1 GI:10610030

KEYWORDS
GSS.
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
1 (bases 1 to 50)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0252 row: H column: 23

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 50.

FEATURES

Location/Qualifiers

1..50

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0252H23"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

ORIGIN

Query Match 60.8%; Score 14.6; DB 8; Length 50;
Best Local Similarity 71.4%; Pred. No. 4.5e+04;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCACCAGGCGCUCAGAUAGGA 24
|||||:|||||:|||||:|||||
DB 6 CCACCGGTGCTTCAGCCATGA 26

RESULT 3

AZ452625 42 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
1M0252002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0252002 R, genomic survey sequence.

ACCESSION
AZ452625
VERSION
AZ452625.1 GI:10609621

KEYWORDS
GSS.
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0252 row: O column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 42.

FEATURES

Location/Qualifiers

1..42

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0252002"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 58.3%; Score 14; DB 8; Length 42;
Best Local Similarity 63.6%; Pred. No. 8.4e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 UUCCACGAGGCGCUCAGUAGG 23
:|||||:|:|||||
Db 21 TACCACGAGTCACTTAGACAGG 42

RESULT 4
AZ595168/c
LOCUS
DEFINITION 44 bp DNA linear GSS 13-DEC-2000
1M0407C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0407C07 R, genomic survey sequence.

ACCESSION AZ595168
VERSION AZ595168.1 GI:11717358
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 44)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0407 row: C column: 07
Seq primer: CACACAGGAGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 44.

FEATURES

source
1..44
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0407C07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 58.3%; Score 14; DB 8; Length 44;
Best Local Similarity 59.1%; Pred. No. 8.5e+04;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCGCUCAGUAG 22
:|||||:|:|||||
Db 35 ATTCAACGAGTGGCTCGCACAG 14

RESULT 5
BF143628/c
LOCUS
DEFINITION 57 bp mRNA linear EST 24-OCT-2000
601790985F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021725 5',
mRNA sequence.

ACCESSION BF143628
VERSION BF143628.1 GI:10982668
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 57)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9277 row: i column: 22
High quality sequence stop: 57.

FEATURES

source
1..57
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4021725"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 58.3%; Score 14; DB 2; Length 57;
Best Local Similarity 78.6%; Pred. No. 8.8e+04;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCCACGAGGCGCUC 16
:|||||:|:|||||
Db 52 TCCACGAGTGGCTC 39

RESULT 6
AI327266
LOCUS
DEFINITION 58 bp mRNA linear EST 23-DEC-1998
m005a08.x1 Stratagene mouse lung 937302 Mus musculus cDNA clone
IMAGE:552662 3' similar to SW:IF3X_HUMAN P55884 EUKARYOTIC
TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT 1; mRNA sequence.

```

ACCESSION   AI327266
VERSION     AI327266.1  GI:4061695
KEYWORDS    EST
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 58)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geiseli,S., Kucaba,T., Lucy,M., Le,M., Martin,J., Morris,M.,
            Schellberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE       The WashU-HMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LML ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:333454
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            High quality sequence stop: 1.
FEATURES             1..58
                     Location/Qualifiers
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="C57BL/6 x CBA"
                        /db_xref="taxon:10090"
                        /clone="IMAGE:552662"
                        /sex="female"
                        /tissue_type="lung"
                        /dev_stage="6-8 month old"
                        /lab_host="SOLR (kanamycin resistant)"
                        /clone_lib="Stratagene mouse lung 937302"
                        /notes="Organ: lung; Vector: pBluescript SK-; Site 1:
                        ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
                        Oligo dt. 6-8 month old female lung and 1.5 year old male
                        lung were source of mRNA. Average insert size: 1.5 kb;
                        Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG
                        3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
ORIGIN
Query Match       57.5%; Score 13.8; DB 1; Length 58;
Best Local Similarity 70.8%; Pred. No. 1.1e+05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3  UCCACCAGUGCCUCACAGA 19
        :|||||:|||||:
Db      6  TCCACCATTGCCTCAGA 22

RESULT 7
AZ588961/c
LOCUS      33 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0397C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0397C07 R, genomic survey sequence.
ACCESSION  AZ588961
VERSION     AZ588961.1  GI:11711151
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0397 row: C column: 07
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
FEATURES             1..33
                     Location/Qualifiers
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UUGC1M0397C07"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                        /note="Vector: PWD42nv; Purified genomic DNA from M.
                        musculus C57BL/6J (male) was obtained from the Jackson
                        Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/). The DNA
                        was hydrodynamically sheared by repeated passage through a
                        0.005 inch orifice at constant velocity. The sheared DNA
                        was blunt end-repaired with T4 DNA polymerase and T4
                        polynucleotide kinase. Adaptor oligonucleotides were
                        ligated to the blunt ends in high molar excess. The
                        adaptor DNA was purified and size-selected for a 9.5 to
                        10.5 kb range using preparative agarose gel
                        electrophoresis. Vector DNA was prepared from a derivative
                        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                        inducible derivative of plasmid R1. The vector was ligated
                        with adaptors complementary to the insert adaptors and
                        purified. The sheared, adaptor mouse DNA was annealed to
                        adaptor vector DNA, and transformed into
                        chemically-competent E. coli XL10-Gold (Stratagene) cells
                        and selected for ampicillin resistance."
ORIGIN
Query Match       56.7%; Score 13.6; DB 8; Length 33;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2  UUCCACCAGUGCCUCACAGA 21
        :|||||:|||||:
Db      22  TTCCCCCATAGGCTCAGATA 3

RESULT 8
BH851910/c
LOCUS      30 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK 073697.35,80.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_073697.35.80.x, genomic
            survey sequence.
ACCESSION  BH851910
VERSION     BH851910.1  GI:21422781
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

```

REFERENCE
AUTHORS
  Alonso,J.M., Leisese,T.J., Barajas,P., Chen,H., Cheuk,R.,
  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
  Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
JOURNAL
COMMENT
  Contact: Joseph R. Ecker
  Salk Institute Genomic Analysis Laboratory (SIGAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: ecker@salk.edu
  This is single pass sequence recovered from the left border of
  TDNA. This sequence lies within an annotated exon of At4G25180.
  Class: TDNA tagged.
FEATURES
  source
    1..30
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /ecotype="Col-0"
    /db_xref="taxon:3702"
    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
    /note="PCR was performed on Arabidopsis thaliana lines
    each of which contains one or more TDNA insertion
    elements. The resultant fragment for each line was
    directly sequenced to determine the genomic sequence at
    the site of insertion. Details of the protocols used can
    be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
  Query Match 55.8%; Score 13.4; DB 8; Length 30;
  Best Local Similarity 56.5%; Pred. No. 1.5e+05;
  Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
  QY 1 AUUCCACGAGUCGUCUACGAGG 23
  Db 29 ATTCCACACACAGTTTCAGATAG 7
  RESULT 9
  CL903303
  LOCUS
  DEFINITION
    CL903303 51 bp mRNA linear GSS 01-SEP-2004
  ACCESSION
    CL903303.1 GI:51832649
  VERSION
  KEYWORDS
  SOURCE
  ORGANISM
    Mus musculus (house mouse)
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 51)
  http://baygenomics.ucsf.edu/
  Unpublished (2001)
  Contact: BayGenomics
  Bay Area Functional Genomics Consortium (BayGenomics)
  Email: info@baygenomics.ucsf.edu
  Sequence tag generated by 5' RACE of total RNA from gene trap ES
  cell line. ES cell lines harboring insertion mutation of target
  gene are available upon request from BayGenomics. Annotation
  information available from
  http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
  CELL_LINE&KEY=RRX310
  Class: Gene trap.
FEATURES
  source
    1..51
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="129 Ola"

```

```

/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT2Lxf"
/note="Vector: pGT2Lxf"
ORIGIN
  Query Match 55.8%; Score 13.4; DB 9; Length 51;
  Best Local Similarity 56.5%; Pred. No. 1.7e+05;
  Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
  QY 2 UUCCACGAGUCGUCUACGAGGA 24
  Db 4 TTCTATCAGTCCTCCATGAGGA 26
  RESULT 10
  BZ660828
  LOCUS
  DEFINITION
    BZ660828 56 bp DNA linear GSS 31-JAN-2003
    SALK_024289.23.50.x Arabidopsis thaliana TDNA insertion lines
    Arabidopsis thaliana genomic clone SALK_024289.23.50.x, genomic
    survey sequence.
  ACCESSION
    BZ660828
  VERSION
    BZ660828.1 GI:28173975
  KEYWORDS
  SOURCE
  ORGANISM
    Arabidopsis thaliana (chale cress)
    Arabidopsis thaliana
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  1 (bases 1 to 56)
  Alonso,J.M., Leisese,T.J., Barajas,P., Chen,H., Cheuk,R.,
  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
  Shinn,P., Zimmerman,J. and Ecker,J.R.
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
  Unpublished (2001)
  Contact: Joseph R. Ecker
  Salk Institute Genomic Analysis Laboratory (SIGAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: ecker@salk.edu
  This is single pass sequence recovered from the left border of
  TDNA. This sequence lies within an annotated intron of At1g04870.
  Class: TDNA tagged.
FEATURES
  source
    1..56
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /ecotype="Col-0"
    /db_xref="taxon:3702"
    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
    /note="PCR was performed on Arabidopsis thaliana lines
    each of which contains one or more TDNA insertion
    elements. The resultant fragment for each line was
    directly sequenced to determine the genomic sequence at
    the site of insertion. Details of the protocols used can
    be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
  Query Match 55.8%; Score 13.4; DB 8; Length 56;
  Best Local Similarity 56.5%; Pred. No. 1.7e+05;
  Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
  QY 2 UUCCACGAGUCGUCUACGAGGA 24
  Db 33 TTCCTCCAGTCCAGTTATAGAA 55
  RESULT 11

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AI443458/c
LOCUS      31 bp      mRNA      linear      EST 23-JUL-2004
DEFINITION      Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
PROTEIN ;, mRNA sequence.
ACCESSION      AI443458
VERSION        AI443458.1 GI:4303310
KEYWORDS       Glycine max (soybean)
SOURCE         Glycine max
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE      1 (bases 1 to 31)
AUTHORS        Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
PUBLISHED      Public Soybean EST Project
CONTACT        Shoemaker R/Public Soybean EST Project
INSTITUTION    Public Soybean EST Project
WASHINGTON      Washington University School of Medicine
ADDRESS        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL            Tel: 314 286 1800
FAX            Fax: 314 286 1810
EMAIL          Email: est@watson.wustl.edu
NOTES          When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Trace
considered overall poor quality Possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
4163; email: info@biogeneticservices.com)
SEQ PRIMER     Seq primer: -40RP from Gibco
HIGH QUALITY   High quality sequence stop: 1
POLYA=No.      Location/Qualifiers
1..31
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1004-1144"
/tissue_type="root"
/lab_host="XL10-Gold"
/clone_lib="Gm-c1004"
/notes="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First- strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
Stratagene's first-strand synthesis primer was used
[GAGAGAGAGAGAGAGAACTAGTCGAG(T)-18]. After
second-strand synthesis, the cDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were
size-fractionated with a 500bp cutoff, using GibcoBRL Life
Technologies' cDNA Size Fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+)) that had been
digested with EcoRI and XhoI, and phosphorylated). Both
the white and blue colonies appear to contain recombinant
plasmids with cDNA inserts. Blue colonies 9n=15) have been
sequenced, and possess putative cDNA inserts. This library
was constructed by Dr. Paul Keim & Virginia H. Coryell,

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Department of Biology, Box5640, Northern Arizona
University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
520-523-7500, email: paul.keim@nau.edu,
virginia.coryell@nau.edu"

ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 31;
Best Local Similarity 72.2%; Pred. No. 1.9e+05;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      6 ACACGUGCCUCACAGUAGG 23
        |||||:||||:||||
Db      28 ACCAGTGC CGGTGATAGG 11

RESULT 12
AZ604085/c
LOCUS      41 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION      IM0423G16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0423G16 R, genomic survey sequence.
ACCESSION      AZ604085
VERSION        AZ604085.1 GI:11726275
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
UNPUBLISHED    Unpublished (2000)
CONTACT        Contact: Robert B. Weiss
INSTITUTION    University of Utah Genome Center
ADDRESS        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
TEL            Tel: 801 585 5606
FAX            Fax: 801 585 7177
EMAIL          Email: ddunn@genetics.utah.edu
INSERT LENGTH  Insert Length: 10000 Std Error: 0.00
PLACE         Place: 0423 row: G column: 16
SEQ PRIMER     Seq primer: CACACAGAAACAGCTATGACC
CLASS          Class: plasmid ends
HIGH QUALITY   High quality sequence stop: 41.
Location/Qualifiers
1..41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0423G16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

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with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN
Query Match      55.0%; Score 13.2; DB 8; Length 41;
Best Local Similarity 61.1%; Pred. No. 2e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AUUCCAGCAGGCGCCACAG 18
Db 28 ATTCCAGCAGTGCATTCAG 11

RESULT 13
LOCUS AA782065/c
DEFINITION aa782065.1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
CYTIDYLYLTRANSFERASE 1, mRNA sequence.
ACCESSION AA782065
VERSION AA782065.1 GI:28411396
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 52)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 2110 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..52
/organism="Homo sapiens"
/db_type="mRNA"
/db_xref="taxon:9606"
/clone="1360121"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares parathyroid tumor NbHPA"
/notes="Organ: parathyroid gland; Vector: pTTT3D
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCACCAATTTTTTTTTTTTTTTT
TTTTT-3'] double-stranded cDNA was size selected, ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pTT3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

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ORIGIN

Query Match 55.0%; Score 13.2; DB 1; Length 52;
Best Local Similarity 61.1%; Pred. No. 2.1e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 UCCACCAGGCGCCACAG 20
Db 23 TTCCCGGTGCCTCAGAT 6

RESULT 14

CL522553

LOCUS

DEFINITION

CL522553 SAM6B01 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines
Oryza sativa (japonica cultivar-group) genomic, genomic survey
sequence.

ACCESSION

CL522553

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 52)

AUTHORS

Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanelli, P., Piegou, B.,
Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C.,
Ghesquiere, A., Delsen, M., Glaszmann, J.C. and Guiderdoni, E.

TITLE

High throughput T-DNA insertion mutagenesis in rice: A first step
towards in silico reverse genetics

JOURNAL

Plant J. (2004) In press

COMMENT

Contact: Guiderdoni
UMR PIA Biotrop program
CIRAD

TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE

Tel: 33467615629

Fax: 33467615605

Email: emmanuel.guiderdoni@cirad.fr

Class: TDNA tagged.

FEATURES

Location/Qualifiers

1..52

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone_lib="Planking Sequence Tag of Oryza sativa T-DNA
insertion lines"/note="PCR was performed on DNA of primary transformants
of Oryza sativa plants. The DNA fragment(s) resulting of
PCR were directly sequenced from the left border to
determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed. Information to order
the corresponding mutant line and a link to a database
providing a graphical display is available from June 2004
at <http://genoplante-info.infobiogen.fr/oryzatagline/>.
This sequence has been generated in the framework of the
French plant genomics program Genoplante
(<http://www.genoplante.org> and
<http://genoplante-info.infobiogen.fr>)."

ORIGIN

Query Match 55.0%; Score 13.2; DB 9; Length 52;
Best Local Similarity 66.7%; Pred. No. 2.1e+05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 UCCACCAGGCGCCACAG 20
Db 5 TCCACCAGTGCACAGAT 22

RESULT 15

CC178725

LOCUS CC178725 53 bp mRNA linear GSS 02-MAY-2003
DEFINITION XA060 BayGenomics Gene Trap Library pGT0pfs Mus musculus CDNA, mRNA
sequence.
ACCESSION CC178725
VERSION CC178725.1 GI:30317276
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 53)
AUTHORS BayGenomics.
TITLE http://baygenomics.ucsf.edu/
JOURNAL Unpublished (2001)
COMMENT Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XA060
Class: Gene Trap.
Location/Qualifiers
1..53
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0pfs"
/note="Vector: pGT0pfs"

ORIGIN

Query Match 55.0%; Score 13.2; DB 8; Length 53;
Best Local Similarity 61.1%; Pred. No. 2.1e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 UCCACGAGUGCCUCAGAU 20
:|||||:|||||:
Db 13 TCCAGCTGTGCATCAGAT 30

Search completed: July 30, 2005, 18:20:58
Job time : 2336.57 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	\$				
1	15.6	65.0	30	3	US-08-650-726-2	Sequence 2, Appli	
2	15.4	64.2	20	3	US-09-792-594-41	Sequence 41, Appl	
C 3	15.2	63.3	25	4	US-09-396-196G-1657	Sequence 1657, Ap	
	15.2	63.3	25	4	US-09-396-196G-102634	Sequence 102634, A	
C 5	14.6	60.8	25	4	US-09-396-196G-83857	Sequence 83857, A	
6	14.6	60.8	32	3	US-09-249-585A-12	Sequence 12, Appl	
7	14.2	59.2	24	1	US-08-488-212A-43	Sequence 43, Appl	
8	14.2	59.2	24	2	US-08-320-306-43	Sequence 43, Appl	
9	14.2	59.2	24	2	US-08-488-209B-43	Sequence 43, Appl	
10	14.2	59.2	24	2	US-08-408-011-43	Sequence 43, Appl	
C 11	14.2	59.2	25	4	US-09-396-196G-81072	Sequence 81072, A	
C 12	14.2	59.2	25	4	US-09-396-196G-81073	Sequence 81073, A	
13	14.2	59.2	25	4	US-09-396-196G-102633	Sequence 102633, A	
C 14	14	58.3	25	4	US-09-396-196G-37434	Sequence 37434, A	
	14	58.3	25	4	US-09-396-196G-120549	Sequence 120549, A	
16	14	58.3	46	1	US-07-692-995B-45	Sequence 45, Appl	
C 17	13.8	57.5	20	1	US-08-714-626-3	Sequence 3, Appli	
C 18	13.8	57.5	20	2	US-08-922-169-3	Sequence 3, Appli	
19	13.8	57.5	20	4	US-09-705-267A-107	Sequence 107, App	
C 20	13.8	57.5	20	5	PCR-US95-04852-3	Sequence 3, Appli	
C 21	13.8	57.5	23	3	US-09-124-238A-30	Sequence 30, Appl	
C 22	13.8	57.5	23	3	US-09-721-975-30	Sequence 30, Appl	
C 23	13.8	57.5	23	4	US-09-986-621-30	Sequence 30, Appl	
C 24	13.8	57.5	25	4	US-09-396-196G-119424	Sequence 119424, A	
C 25	13.8	57.5	33	3	US-08-169-715-53	Sequence 53, Appl	
26	13.6	56.7	25	3	US-08-737-607-37	Sequence 37, Appl	
27	13.6	56.7	25	4	US-09-396-196G-64157	Sequence 64157, A	

```
Db      8  TTTCACCTGTGGCTCAGATAGG 29

RESULT 2
US-09-792-594-41
; Sequence 41, Application US/09792594
; Patent No. 6436706
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL4 EXPRESSION
; FILE REFERENCE: RTS-0209
; CURRENT APPLICATION NUMBER: US/09/792,594
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-792-594-41

Query Match      64.2%; Score 15.4; DB 3; Length 20;
Best Local Similarity 76.5%; Pred. No. 3.2e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4  CCACCAGUGCCUCAGAU 20
      |||||:||||:||||:
Db      1  CCACCAGTGCCTCAGGT 17

RESULT 3
US-09-396-196G-1657/c
; Sequence 1657, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1657
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1657

Query Match      63.3%; Score 15.2; DB 4; Length 25;
Best Local Similarity 70.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1  AUUCCACCAGUGCCUCAGAU 20
      |:|||||:||||:
Db      22  ATGCCACGAGTGCACACAGAT 3

RESULT 4
US-09-396-196G-102634
; Sequence 102634, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.

Db      8  TTTCACCTGTGGCTCAGATAGG 29

TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102634
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102634

Query Match      63.3%; Score 15.2; DB 4; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1  AUUCCACCAGUGCCUCAGAU 20
      |::|:||||:|:|:
Db      1  ATTCAACCACTGACTAAGAT 20

RESULT 5
US-09-396-196G-83857/c
; Sequence 83857, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83857
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-83857

Query Match      60.8%; Score 14.6; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      4  CCACCAGUGCCUCAGAUAGGA 24
      |||||:||||:|:|:
Db      22  CCACCTAGTGGTCTGTTAGGA 2

RESULT 6
US-09-249-585A-12
; Sequence 12, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 32
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
```


LOCATION: (1)...(32)
OTHER INFORMATION: oligonucleotide used for RT-PCR amplification of Bcl2
US-09-249-585A-12

Query Match 60.8%; Score 14.6; DB 3; Length 32;
Best Local Similarity 61.9%; Pred. No. 8.7e+02;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 UCCACGAGGCGCCGATAGG 23
DB 12 TTCACCTGTGGCTCAGATAGG 32

RESULT 7
US-08-488-212A-43
Sequence 43, Application US/08488212A
Patent No. 5665355
GENERAL INFORMATION:
APPLICANT: Primi, Daniele
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: AIDS Onset
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas
ADDRESSER: Popovich & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea
COMPUTER: 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,212A
FILING DATE: 07-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,485
FILING DATE: No. 5665355ember 9, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: (oligonucleotide useful in amplification of T Cell Receptor
MOLECULE TYPE: Va region)
HYPOTHETICAL: No
ORIGINAL SOURCE: Synthesized using
ORIGINAL SOURCE: oligonucleotide synthesis machine
PUBLICATION INFORMATION:
AUTHORS: Imberti, Luisa; Sottini,
AUTHORS: Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
AUTHORS: Daniele
TITLE: Selective Depletion in HIV Infection
TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
JOURNAL: Science
VOLUME: 254
ISSUE: 5033
PAGES: 860-862

US-08-488-212A-43
Sequence 43, Application US/08320306
Patent No. 5891623
GENERAL INFORMATION:
APPLICANT: Primi, Daniele
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: AIDS Onset
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas
ADDRESSER: Popovich & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea
COMPUTER: 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,306
FILING DATE: 06-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,485
FILING DATE: No. 5891623ember 9, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: (oligonucleotide useful in amplification of T Cell Receptor
MOLECULE TYPE: Va region)
HYPOTHETICAL: No
ORIGINAL SOURCE: Synthesized using
ORIGINAL SOURCE: oligonucleotide synthesis machine
PUBLICATION INFORMATION:
AUTHORS: Imberti, Luisa; Sottini,
AUTHORS: Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
AUTHORS: Daniele
TITLE: Selective Depletion in HIV Infection
TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
JOURNAL: Science
VOLUME: 254
ISSUE: 5033
PAGES: 860-862


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Query Match      59.2%; Score 14.2; DB 2; Length 24;
Best Local Similarity 68.4%; Pred. No. 1.3e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 AUUCACACGAGCCUCACAGA 19
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Db 5 ATTCACACGAGCCCTCAGA 23

RESULT 11
US-09-396-196G-81072/c
; Sequence 81072, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81072
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-81072

Query Match      59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 CACCAGUGCCUCAGAUAGG 23
    |:|:| |:|:| |:|:| |:|:|
Db 25 CACCAGTTCCACAGATGGG 7

RESULT 12
US-09-396-196G-81073/c
; Sequence 81073, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-81073

Query Match      59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 CACCAGUGCCUCAGAUAGG 23
    |:|:| |:|:| |:|:| |:|:|
Db 19 CACCAGTTCCACAGATGGG 1

RESULT 13
US-09-396-196G-102633
; Sequence 102633, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102633
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102633

Query Match      59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 63.2%; Pred. No. 1.3e+03;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AUUCACACGAGCCUCACAGA 19
    |:|:| |:|:| |:|:| |:|:|
Db 7 ATTCACACGAGTACTACAGA 25

RESULT 14
US-09-396-196G-37454/c
; Sequence 37454, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37454
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-37454

Query Match      58.3%; Score 14; DB 4; Length 25;
Best Local Similarity 63.6%; Pred. No. 1.6e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 UCCACACGAGCCUCAGAUAGGA 24
    |:|:| |:|:| |:|:| |:|:|
Db 23 TCCAGCTGTGTCTCCGAAGGA 2

RESULT 15
US-09-396-196G-120549
; Sequence 120549, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
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; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-120549

Query Match      58.1%; Score 14; DB 4; Length 25;
Best Local Similarity 59.1%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      2 UUCACCCAGUGCCUCAGAUAGG 23
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Db      1 TTCATCCAGTGGCTGAGAGAGG 22

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:29:53 ; Search time 451.784 Seconds
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343.829 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 aauccacaguccuacgauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

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Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	21	87.5	25	21	Sequence 4363, Ap
C 3	21	87.5	25	21	Sequence 183480,
C 4	21	87.5	25	21	Sequence 183481,
C 5	21	87.5	25	21	Sequence 183482,
C 6	21	87.5	25	21	Sequence 183483,
C 7	17	70.8	17	10	Sequence 183484, Ap

C 8	17	70.8	17	10	US-09-780-533A-1534	Sequence 1534, Ap
C 9	17	70.8	17	10	US-09-780-533A-1774	Sequence 1774, Ap
C 10	17	70.8	17	10	US-09-780-533A-2081	Sequence 2081, Ap
C 11	17	70.8	17	10	US-09-780-533A-2693	Sequence 2693, Ap
C 12	17	70.8	25	19	US-10-717-597-4362	Sequence 4362, Ap
C 13	16.2	67.5	25	21	US-10-719-900-292913	Sequence 292913,
C 14	16	66.7	17	10	US-09-780-533A-1532	Sequence 1532, Ap
C 15	16	66.7	17	10	US-09-780-533A-2694	Sequence 2694, Ap
C 16	15.8	65.8	25	21	US-10-719-900-448746	Sequence 448746,
C 17	15.8	65.8	25	21	US-10-719-900-832455	Sequence 832455,
C 18	15.8	65.8	25	22	US-10-719-956-457031	Sequence 457031,
C 19	15.6	65.0	22	19	US-10-316-515-6	Sequence 6, Appli
C 20	15.6	65.0	25	21	US-10-719-900-885669	Sequence 885669,
C 21	15.6	65.0	25	22	US-10-719-956-252140	Sequence 252140,
C 22	15.4	64.2	60	10	US-09-908-975-6841	Sequence 6841, Ap
C 23	15.2	63.3	25	21	US-10-809-189-1657	Sequence 1657, Ap
C 24	15.2	63.3	25	21	US-10-809-189-102634	Sequence 102634,
C 25	15.2	63.3	25	22	US-10-719-956-270018	Sequence 270018,
C 26	15	62.5	17	10	US-09-780-533A-714	Sequence 714, App
C 27	15	62.5	17	10	US-09-780-533A-2082	Sequence 2082, Ap
C 28	15	62.5	25	21	US-10-719-900-747466	Sequence 747466,
C 29	15	62.5	25	22	US-10-719-956-66724	Sequence 66724, A
C 30	15	62.5	25	22	US-10-719-956-71795	Sequence 71795, A
C 31	15	62.5	25	22	US-10-719-956-539128	Sequence 539128,
C 32	15	62.5	50	17	US-10-131-827-660	Sequence 660, App
C 33	14.8	61.7	25	21	US-10-719-900-864194	Sequence 864194,
C 34	14.8	61.7	25	22	US-10-719-956-88068	Sequence 88068, A
C 35	14.8	61.7	25	22	US-10-719-956-516451	Sequence 516451,
C 36	14.6	60.8	25	15	US-10-098-2638-32948	Sequence 32948, A
C 37	14.6	60.8	25	21	US-10-719-900-244717	Sequence 244717,
C 38	14.6	60.8	25	21	US-10-719-900-292914	Sequence 292914,
C 39	14.6	60.8	25	21	US-10-719-900-370596	Sequence 370596,
C 40	14.6	60.8	25	21	US-10-719-900-792127	Sequence 792127,
C 41	14.6	60.8	25	21	US-10-719-900-868576	Sequence 868576,
C 42	14.6	60.8	25	21	US-10-809-189-83857	Sequence 83857, A
C 43	14.6	60.8	25	21	US-10-956-157-300308	Sequence 300308, A
C 44	14.6	60.8	25	22	US-10-719-956-25044	Sequence 25044, A
C 45	14.6	60.8	25	22	US-10-719-956-249546	Sequence 249546,

ALIGNMENTS

RESULT 1
US-10-717-597-4363/c
; Sequence 4363, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trapietto, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10717597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4363
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-4363
Query Match 91.7%; Score 22; DB 19; Length 25;
Best Local Similarity 77.3%; Pred. No. 0.94;

QY 2 UUCACCAGGUCUCAGUAG 22
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Db 25 TTCCACCAGTGCCTCAGATAG 5

RESULT 7
US-09-780-533A-1533/c
; Sequence 1533, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1533
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1533

Query Match 70.8%; Score 17; DB 10; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.5e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCCACCAGGUCUCACAGA 19
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Db 17 TCCACCAGTGCCTCAGA 1

RESULT 8
US-09-780-533A-1534/c
; Sequence 1534, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1534
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1534

Query Match 70.8%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGGUCUCUA 17
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Db 17 ATTCCACCAGTGCCTCA 1

RESULT 9

US-09-780-533A-1774/c
; Sequence 1774, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1774
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1774

Query Match 70.8%; Score 17; DB 10; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.5e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CAGUGCCUCAGAUAGGA 24
|||:||||:||||:|
Db 17 CAGTGCCTCAGATAGGA 1

RESULT 10
US-09-780-533A-2081/c
; Sequence 2081, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2081
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2081

Query Match 70.8%; Score 17; DB 10; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.5e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 CACCAGGUCUCAGAUUA 21
|||:||||:||||:|
Db 17 CACCAGTGCCTCAGATA 1

RESULT 11
US-09-780-533A-2693/c
; Sequence 2693, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim

```
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2693
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2693

Query Match          70.8%; Score 17; DB 10; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.5e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACCAGGCGCCUACAGUAG 22
DB      17 ACCAGTGCCTCAGATAG 1

RESULT 12
US-10-717-597-4362/c
; Sequence 4362, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4362
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-4362

Query Match          70.8%; Score 17; DB 19; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.6e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      8 CAGUGCCUCAGUAGGA 24
DB      25 CAGTGCCTCAGATAGGA 9

RESULT 13
US-10-719-900-292913/c
; Sequence 292913, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
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; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-292913

Query Match          67.5%; Score 16.2; DB 21; Length 25;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 UCCACGAGUGCCUCACAGUAGG 23
DB      25 TCATCATGCTGCCTCACACAGG 5

RESULT 14
US-09-780-533A-1532/c
; Sequence 1532, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1532
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1532

Query Match          66.7%; Score 16; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 7.8e+02;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      9 AGUGCCUCAGUAGGA 24
DB      17 AGTGCCTCAGATAGGA 2

RESULT 15
US-09-780-533A-2694/c
; Sequence 2694, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2694
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
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US-09-780-533A-2694

Query Match 66.7%; Score 16; DB 10; Length 17;
Best Local Similarity 75.0%; Pred. No. 7.8e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATCCACGAGGCTC 16
|:|||||:|:|:|
Db 16 AATCCACGAGGCTC 1

Search completed: July 30, 2005, 18:48:38
Job time : 452.784 secs

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:29:53 ; Search time 470.608 Seconds
(without alignments)
343.829 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacuacaggaucagauagccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 8371272

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*

23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq*

24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*

25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*

26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.6	66.4	25	21 US-10-719-900-329432	Sequence 329432,
2	16.6	66.4	25	21 US-10-719-900-329433	Sequence 329433,
3	16.2	64.8	60	10 US-09-908-975-14572	Sequence 14572, A
C 4	16	64.0	17	10 US-09-780-533A-568	Sequence 568, App
C 5	16	64.0	25	21 US-10-956-157-21957	Sequence 21957, A
C 6	16	64.0	25	21 US-10-956-157-21960	Sequence 21960, A
C 7	16	64.0	25	21 US-10-956-157-97484	Sequence 97484, A

C 8	16	64.0	25	21 US-10-956-157-135597	Sequence 135597,
C 9	16	64.0	40	18 US-10-453-827-239	Sequence 239, App
C 10	16	64.0	60	19 US-10-642-093-46	Sequence 46, Appl
C 11	16	64.0	60	19 US-10-795-002-46	Sequence 46, Appl
C 12	15.6	62.4	25	21 US-10-719-900-41315	Sequence 41315, A
C 13	15.6	62.4	25	21 US-10-956-157-21946	Sequence 21946, A
C 14	15.6	62.4	25	21 US-10-956-157-21947	Sequence 21947, A
C 15	15.6	62.4	25	21 US-10-956-157-21963	Sequence 21963, A
C 16	15.6	62.4	25	21 US-10-956-157-97462	Sequence 97462, A
C 17	15.6	62.4	25	21 US-10-956-157-97463	Sequence 97463, A
C 18	15.6	62.4	25	21 US-10-956-157-179966	Sequence 179966,
C 19	15.6	62.4	25	22 US-10-719-956-618759	Sequence 618759,
C 20	15.4	61.6	25	21 US-10-719-900-895386	Sequence 895386,
C 21	15.4	61.6	25	22 US-10-719-956-269689	Sequence 269689,
C 22	15.4	61.6	25	22 US-10-719-956-441174	Sequence 441174,
C 23	15.2	60.8	25	22 US-10-719-956-578410	Sequence 578410,
C 24	15	60.0	17	10 US-09-780-533A-567	Sequence 567, App
C 25	15	60.0	17	10 US-09-780-533A-1442	Sequence 1442, Ap
C 26	15	60.0	25	21 US-10-719-900-168271	Sequence 168271,
C 27	15	60.0	25	21 US-10-719-900-581175	Sequence 581175,
C 28	15	60.0	25	21 US-10-719-900-876063	Sequence 876063,
C 29	15	60.0	25	21 US-10-809-189-88973	Sequence 88973, A
C 30	15	60.0	25	22 US-10-719-956-72988	Sequence 72988, A
C 31	15	60.0	60	10 US-09-908-975-6447	Sequence 6447, Ap
C 32	14.8	59.2	23	19 US-10-627-253A-30	Sequence 30, Appl
C 33	14.6	58.4	21	20 US-10-751-736-25240	Sequence 25240, A
C 34	14.6	58.4	21	20 US-10-751-736-25351	Sequence 25351, A
C 35	14.6	58.4	25	21 US-10-719-900-292748	Sequence 292748,
C 36	14.6	58.4	25	21 US-10-719-900-613272	Sequence 613272,
C 37	14.6	58.4	25	21 US-10-719-900-614140	Sequence 614140,
C 38	14.6	58.4	25	21 US-10-719-900-630466	Sequence 630466,
C 39	14.6	58.4	25	21 US-10-719-900-630467	Sequence 630467,
C 40	14.6	58.4	25	21 US-10-956-157-21945	Sequence 21945, A
C 41	14.6	58.4	25	21 US-10-956-157-97461	Sequence 97461, A
C 42	14.6	58.4	25	22 US-10-719-956-38250	Sequence 38250, A
C 43	14.6	58.4	25	22 US-10-719-956-66979	Sequence 66979, A
C 44	14.6	58.4	25	22 US-10-719-956-347262	Sequence 347262,
C 45	14.6	58.4	25	22 US-10-719-956-347263	Sequence 347263,

ALIGNMENTS

RESULT 1

US-10-719-900-329432
; Sequence 329432, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329432
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-329432

Query Match 66.4%; Score 16.6; DB 21; Length 25;
Best Local Similarity 60.9%; Pred. No. 6.4e+02;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGAUUCCAGAUUCC 23

DB 1 CATCTCCGATCCTAGATATGC 23

RESULT 2

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US-10-719-900-329433
; Sequence 329433, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329433
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-329433

Query Match      66.4%; Score 16.6; DB 21; Length 25;
Best Local Similarity 60.9%; Pred. No. 6.4e+02;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAACUUCAGGAUCCAGAUAGCC 23
Db      1 CATCTCCGGATGCTAGATATGC 23

RESULT 3
US-09-908-975-14572/c
; Sequence 14572, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14572
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-14572

Query Match      64.8%; Score 16.2; DB 10; Length 60;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      5 UUCAGGAUCCAGAUAGCC 25
Db      23 TTCACGGTCCAGATATTTCCC 3

RESULT 4
US-09-780-533A-568/c
; Sequence 568, Application US/09780533A
; Publication No. US2003006011A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
```

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; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 568
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-568

Query Match      64.0%; Score 16; DB 10; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      10 GAUUCACAGAUAGCCC 25
Db      16 GATTCAGATATGCC 1

RESULT 5
US-10-956-157-21957/c
; Sequence 21957, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21957
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21957

Query Match      64.0%; Score 16; DB 21; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAACUUCAGGAUCCAGAUAGCC 24
Db      24 CCATCCAGGATGTCAGATATGAC 1

RESULT 6
US-10-956-157-21960/c
; Sequence 21960, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21960
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21960
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Query Match      64.0%; Score 16; DB 21; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGCC 24
   |||:|||||:|||||:|
Db 25 CCACTCCAGGATGTCAGATATGAC 2

RESULT 7
US-10-956-157-97484/c
; Sequence 97484, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97484

Query Match      64.0%; Score 16; DB 21; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGCC 24
   |||:|||||:|||||:|
Db 24 CCACTCCAGGATGTCAGATATGAC 1

RESULT 8
US-10-956-157-135597/c
; Sequence 135597, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 135597
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-135597

Query Match      64.0%; Score 16; DB 21; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAUUCAGAUAGCC 25
   |||:|||||:|||||:|
Db 17 GATTCCAGATATGCC 2

RESULT 9
US-10-453-827-239/c
; Sequence 239, Application US/10453827
; Publication No. US20040033582A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
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; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0211 NP
; CURRENT APPLICATION NUMBER: US/10/453,827
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: U.S. 60/384,980
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 1219
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-453-827-239

Query Match      64.0%; Score 16; DB 18; Length 41;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUAGCC 25
   |||:|||||:|||||:|
Db 34 AACTACAGGATTACACATCTGTCC 11

RESULT 10
US-10-642-093-46
; Sequence 46, Application US/10642093
; Publication No. US20040106555A1
; GENERAL INFORMATION:
; APPLICANT: German, Michael S.
; APPLICANT: Lin, Joseph
; TITLE OF INVENTION: NEUROGENIN3 AND PRODUCTION OF PANCREATIC
; TITLE OF INVENTION: ISLET CELLS
; FILE REFERENCE: UCSF-129CIP2
; CURRENT APPLICATION NUMBER: US/10/642,093
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/US02/11165
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 09/817,360
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 09/535,145
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/128,180
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-642-093-46

Query Match      64.0%; Score 16; DB 19; Length 60;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUAGCC 25
   |||:|||||:|||||:|
Db 2 ATCTTCGGGATCCAGCTGTGTGCC 25

RESULT 11
US-10-795-002-46
; Sequence 46, Application US/10795002
; Publication No. US20040152168A1
; GENERAL INFORMATION:
; APPLICANT: German, Michael S.
; APPLICANT: Lin, Joseph
; TITLE OF INVENTION: NEUROGENIN3 AND PRODUCTION OF PANCREATIC
; TITLE OF INVENTION: ISLET CELLS
; FILE REFERENCE: UCSF-129CIP2
; CURRENT APPLICATION NUMBER: US/10/795,002
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, CURRENT FILING DATE: 2004-03-03
, PRIOR FILING DATE: 2003-08-14
, PRIOR APPLICATION NUMBER: US/10/642,093
, PRIOR FILING DATE: 2003-08-14
, PRIOR APPLICATION NUMBER: PCT/US02/11166
, PRIOR FILING DATE: 2002-03-20
, PRIOR APPLICATION NUMBER: US 09/817,360
, PRIOR FILING DATE: 2001-03-20
, PRIOR APPLICATION NUMBER: US 09/535,145
, PRIOR FILING DATE: 2000-03-24
, PRIOR APPLICATION NUMBER: US 60/128,180
, PRIOR FILING DATE: 1999-04-06
, NUMBER OF SEQ ID NOS: 51
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 46
, LENGTH: 60
, TYPE: DNA
, ORGANISM: Artificial Sequence
, FEATURE:
, -OTHER INFORMATION: oligonucleotide
US-10-795-002-46

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Query Match      64.0%; Score 16; DB 19; Length 60;
Best Local Similarity 59.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY  2 AACUUCAGGAUUCUCCAGAUUGCCC 25
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Db  2 ATCTTCGGATCCAGCTGTGCCC 25

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RESULT 12
US-10-719-900-41315
; Sequence 41315, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41315
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-41315

```

```

Query Match      62.4%; Score 15.6; DB 21; Length 25;
Best Local Similarity 59.1%; Fred. No. 1.9e+03;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0
Qy      2 AACUUCAGGAUCCAGAUAGC 23
Db      1 AACTTAAGTATTCAGCCCATGC 22

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```

RESULT 13
US-10-956-157-21946/c
; Sequence 21946, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAY
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 1010
; CURRENT APPLICATION NUMBER: US/10/956,
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent In version 3.2

```

```

; SEQ ID NO 21946
;
; LENGTH: 25
;
; TYPE: DNA
;
; ORGANISM: Probe Sequence
US-10-956-157-21946

```

```

Query Match      62.4%; Score 15.6; DB 21; Length 25;
Best Local Similarity 63.6%; Pred. No. 1.9e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1  CAACUUCAGGAUUCGAAUG 22
        | | | | | | | | | |
Db      22  CCACTCCAGGATGTCAGATATG 1

```

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RESULT 14
US-10-956-157-21947/c
; Sequence 21947, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAY
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 1010
; CURRENT APPLICATION NUMBER: US/10/956,
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21947
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21947

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Query Match	62.4%	Score 15.6;	DB 21;	Length 25;
Best Local Similarity	63.6%;	Pred. No. 1.9e+03;		
Matches 14;	Conservative 4;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1	CAACUUCAGGAUCCAGAAUG	22	
DB	23	CCACTCCAGGATGTCCAGATATG	2	

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RESULT 15
US-10-956-157-21963/c
; Sequence 21963, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAY
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 10.10)
; CURRENT APPLICATION NUMBER: US/10/956,
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21963
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21963

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Query Match	62.4%	Score 15.6	DB 21	Length 25
Best Local Similarity	63.6%	Fed: No. 1.9e+03		
Matches 14	Conservative 4	Mismatches 4	Indels 0	Gaps 0
QY	3	ACTUCAGGAUUCGAGUAUGCC	24	
Db	24	ACTCCAGGATGTCAGATATGAC	3	

Search completed: July 30, 2005, 18:48:37
Job time : 471.608 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:29:53 ; Search time 470.608 Seconds

(without alignments)
343.829 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

Sequence: 1 cuggaugcuggaucacaccuug 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 8371272

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	25	21	US-10-956-157-169389
C 2	24	96.0	25	21	US-10-719-900-63085, A
C 3	24	96.0	25	21	Sequence 169389, A
C 4	24	96.0	25	21	Sequence 63085, A
C 5	24	96.0	25	21	Sequence 164478, A
C 6	24	96.0	25	21	Sequence 164479, A
C 7	24	96.0	25	21	Sequence 164480, A
C 8	24	96.0	25	21	Sequence 164481, A
C 9	24	96.0	25	21	Sequence 164482, A

C 8	22.4	89.6	25	21	US-10-719-900-63086	Sequence 63086, A
C 9	19.8	79.2	25	22	US-10-719-956-169644	Sequence 169644, A
C 10	18.2	72.8	25	22	US-10-719-956-169643	Sequence 169643, A
C 11	17.2	68.8	25	21	US-10-956-157-158471	Sequence 158471, A
C 12	17	68.0	17	10	US-09-780-533A-561	Sequence 561, App
C 13	17	68.0	17	10	US-09-780-533A-1429	Sequence 1429, App
C 14	17	68.0	17	10	US-09-780-533A-1430	Sequence 1430, App
C 15	17	68.0	17	10	US-09-780-533A-1737	Sequence 1737, App
C 16	17	68.0	17	10	US-09-780-533A-2029	Sequence 2029, App
C 17	17	68.0	17	10	US-09-780-533A-2284	Sequence 2284, App
C 18	16.6	66.4	25	22	US-10-719-956-146225	Sequence 146225, A
C 19	16.4	65.6	22	19	US-10-384-339C-172	Sequence 172, App
C 20	16.4	65.6	24	19	US-10-384-339C-173	Sequence 173, App
C 21	16	64.0	17	10	US-09-780-533A-2028	Sequence 2028, App
C 22	16	64.0	25	21	US-10-956-157-238770	Sequence 238770, A
C 23	15.8	63.2	60	10	US-09-908-975-5561	Sequence 5561, App
C 24	15.6	62.4	25	21	US-10-719-900-195537	Sequence 195537, A
C 25	15.6	62.4	25	22	US-10-719-956-123417	Sequence 123417, A
C 26	15.4	61.6	17	10	US-09-848-754A-931	Sequence 931, App
C 27	15.4	61.6	17	10	US-09-848-754A-934	Sequence 934, App
C 28	15.4	61.6	20	17	US-10-380-931-38	Sequence 38, Appl
C 29	15.2	60.8	25	21	US-10-719-900-115543	Sequence 115543, A
C 30	15.2	60.8	25	21	US-10-719-900-392915	Sequence 392915, A
C 31	15.2	60.8	25	22	US-10-719-956-521423	Sequence 521423, A
C 32	15	60.0	17	10	US-09-780-533A-1431	Sequence 1431, App
C 33	15	60.0	25	21	US-10-719-900-602483	Sequence 602483, A
C 34	15	60.0	25	22	US-10-719-956-146226	Sequence 146226, A
C 35	15	60.0	25	22	US-10-719-956-377866	Sequence 377866, A
C 36	15	60.0	25	22	US-10-719-956-575601	Sequence 575601, A
C 37	15	60.0	60	10	US-09-908-975-7591	Sequence 7591, App
C 38	15	60.0	60	10	US-09-908-975-20410	Sequence 20410, A
C 39	15	60.0	60	21	US-10-764-420-3553	Sequence 3553, App
C 40	15	60.0	60	21	US-10-764-420-3604	Sequence 3604, App
C 41	14.8	59.2	25	21	US-10-719-900-619461	Sequence 619461, A
C 42	14.8	59.2	25	22	US-10-719-956-302908	Sequence 302908, A
C 43	14.8	59.2	25	22	US-10-719-956-412824	Sequence 412824, A
C 44	14.6	58.4	25	21	US-10-719-900-73849	Sequence 73849, A
C 45	14.6	58.4	25	21	US-10-719-900-851430	Sequence 851430, A

ALIGNMENTS

RESULT 1
US-10-956-157-169389/c
; Sequence 169389, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-169389

Query Match 100.0%; Score 25; DB 21; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.034; Indels 0; Gaps 0;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUGCUGGAUCACACCCUUG 25
Db 25 CTGGATAGCTTGGATCACACCCCTTG 1

RESULT 2

1

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; Sequence 164482, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164482
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-164482

Query Match      96.0%; Score 24; DB 21; Length 25;
Best Local Similarity 70.8%; Pred. No. 0.1;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CUGGAUAGCUUGGAUCACACCCUU 24
Db      24  CTGGATAGCTTGGATCACACCCTT 1

RESULT 8
US-10-719-900-63086/c
; Sequence 63086, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 63086
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-63086

Query Match      89.6%; Score 22.4; DB 21; Length 25;
Best Local Similarity 66.7%; Pred. No. 0.63;
Matches 16; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CUGGAUAGCUUGGAUCACACCCUU 24
Db      24  CTGGATAGCTTGGATCACACCCTT 1

RESULT 9
US-10-719-956-169644/c
; Sequence 169644, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169644
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Rattus norvegicus
US-10-719-956-169644

Query Match      79.2%; Score 19.8; DB 22; Length 25;
Best Local Similarity 65.2%; Pred. No. 12;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy      2  UGGAUAGCUUGGAUCACACCCUU 24
Db      25  TGGATAGCTTGGATCACGCCCTT 3

RESULT 10
US-10-719-956-169643/c
; Sequence 169643, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-169643

Query Match      72.8%; Score 18.2; DB 22; Length 25;
Best Local Similarity 60.9%; Pred. No. 69;
Matches 14; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      2  UGGAUAGCUUGGAUCACACCCUU 24
Db      25  TGGATAGCTTGGTTCACGCCCTT 3

RESULT 11
US-10-956-157-158471/c
; Sequence 158471, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-158471

Query Match      68.8%; Score 17.2; DB 21; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      3  GGAUAGCUUGGAUCACACCCUU 24
Db      22  GGACAGCTTGGATCACACTTTT 1

RESULT 12
US-09-780-533A-561/c
; Sequence 561, Application US/09780533A
```

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; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 561
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-561

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      5 AUAGCUUGGAUCACACC 21
Db      17 ATAGCTTGGATCACAC 1

RESULT 13
US-09-780-533A-1429/c
; Sequence 1429, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1429
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1429

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAUAGCUUGGAUCACAC 20
Db      17 GATAGCTTGGATCACAC 1

RESULT 14
US-09-780-533A-1430/c
; Sequence 1430, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1430
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1430

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      8 GCUUGGAUCACACCCU 24
Db      17 GCTTGGATCACACCC 1

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Job time : 471.608 secs

; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1430
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1430

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGAUAGCUUGGAUCACA 19
Db      17 GGATAGCTTGGATCACAC 1

RESULT 15
US-09-780-533A-1737/c
; Sequence 1737, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1737
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1737

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.5e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      8 GCUUGGAUCACACCCU 24
Db      17 GCTTGGATCACACCC 1

Search completed: July 30, 2005, 18:48:36
Job time : 471.608 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:02:47 ; Search time 463.784 Seconds
(without alignments)
334.933 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 auuaccacgucucagauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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- 22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	24	100.0	144	18	US-10-085-783A-33274 Sequence 33274, A
C 3	24	100.0	170	17	US-10-242-535A-57815 Sequence 57815, A
C 4	24	100.0	170	18	US-10-085-783A-57815 Sequence 57815, A
C 5	24	100.0	191	17	US-10-242-535A-28762 Sequence 28762, A
C 6	24	100.0	191	18	US-10-085-783A-28762 Sequence 28762, A
C 7	24	100.0	370	17	US-10-242-535A-54131 Sequence 54131, A

C 8	24	100.0	370	18	US-10-085-783A-54131 Sequence 54131, A
C 9	24	100.0	468	17	US-10-242-535A-31372 Sequence 31372, A
C 10	24	100.0	468	18	US-10-085-783A-31372 Sequence 31372, A
C 11	24	100.0	972	17	US-10-437-931-1 Sequence 1, Appli
C 12	24	100.0	1610	9	US-09-765-205-5 Sequence 5, Appli
C 13	24	100.0	1610	21	US-10-347-669-5 Sequence 52, Appli
C 14	24	100.0	1785	17	US-10-439-388-62 Sequence 62, Appli
C 15	24	100.0	1785	21	US-10-956-157-1705 Sequence 1705, Ap
C 16	24	100.0	2235	14	US-10-060-036-54 Sequence 54, Appli
C 17	24	100.0	4053	9	US-09-758-140-5 Sequence 5, Appli
C 18	24	100.0	4053	9	US-09-972-599A-5 Sequence 5, Appli
C 19	24	100.0	4053	19	US-10-717-597-310 Sequence 310, App
C 20	24	100.0	4532	14	US-10-060-036-53 Sequence 53, Appli
C 21	24	100.0	4710	10	US-09-764-891-7385 Sequence 7385, Ap
C 22	22	91.7	25	19	US-10-717-597-4363 Sequence 4363, Ap
C 23	22	91.7	211	14	US-10-004-427-51 Sequence 51, Appli
C 24	22	91.7	211	21	US-10-984-752-51 Sequence 51, Appli
C 25	22	91.7	360	9	US-09-764-846-60 Sequence 60, Appli
C 26	22	91.7	360	14	US-10-091-483-60 Sequence 60, Appli
C 27	22	91.7	377	9	US-09-764-846-132 Sequence 132, App
C 28	22	91.7	377	14	US-10-091-483-132 Sequence 132, App
C 29	22	91.7	410	10	US-09-918-995-22263 Sequence 22263, A
C 30	22	91.7	602	20	US-10-357-930-49749 Sequence 49749, A
C 31	22	91.7	633	20	US-10-357-930-19960 Sequence 19960, A
C 32	22	91.7	994	11	US-09-978-360A-110 Sequence 110, App
C 33	22	91.7	1160	14	US-10-175-523-156 Sequence 156, App
C 34	22	91.7	1400	21	US-10-956-157-9762 Sequence 9762, Ap
C 35	22	91.7	1400	21	US-10-956-157-9763 Sequence 9763, Ap
C 36	22	91.7	1400	21	US-10-956-157-9765 Sequence 9765, Ap
C 37	22	91.7	1400	21	US-10-956-157-9766 Sequence 9766, Ap
C 38	22	91.7	1400	21	US-10-956-157-9767 Sequence 9767, Ap
C 39	22	91.7	1514	9	US-09-823-245A-349 Sequence 349, App
C 40	22	91.7	1609	21	US-10-956-157-4527 Sequence 4527, Ap
C 41	22	91.7	1798	19	US-10-466-258-10 Sequence 10, Appli
C 42	22	91.7	1798	22	US-10-466-391A-10 Sequence 10, Appli
C 43	22	91.7	1980	17	US-10-220-891-22 Sequence 22, Appli
C 44	22	91.7	2050	21	US-10-956-157-4530 Sequence 4530, Ap
C 45	22	91.7	2052	19	US-10-466-258-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-242-535A-33274/c
; Sequence 33274, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33274
; LENGTH: 144
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-33274

Query Match 100.0%; Score 24; DB 17; Length 144;
Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AUUCCACGAGGCGCTCAGATAGGA 24
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Db 69 ATTCCACGAGTGCCTCAGATAGGA 46

RESULT 2
US-10-085-783A-33274/c
; Sequence 33274, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33274
; LENGTH: 144
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-33274

Query Match 100.0%; Score 24; DB 18; Length 144;
Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGGCGCTCAGATAGGA 24
   |:|||||:|:|:|:|:|:|:|:|:|
Db 69 ATTCCACGAGTGCCTCAGATAGGA 46

RESULT 3
US-10-242-535A-57815/c
; Sequence 57815, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57815
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57815

Query Match 100.0%; Score 24; DB 17; Length 170;
Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGGCGCTCAGATAGGA 24
   |:|||||:|:|:|:|:|:|:|:|:|
Db 116 ATTCCACGAGTGCCTCAGATAGGA 93

RESULT 4
US-10-085-783A-57815/c
; Sequence 57815, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57815
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57815

Query Match 100.0%; Score 24; DB 18; Length 170;
Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGGCGCTCAGATAGGA 24
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Db 97 ATTCCACGAGTGCCTCAGATAGGA 74

RESULT 5
US-10-242-535A-28762/c
; Sequence 28762, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28762
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-28762

Query Match 100.0%; Score 24; DB 17; Length 191;
Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGGCGCTCAGATAGGA 24
   |:|||||:~|:~|:~|:~|:~|:~|:~|:~|:~|
Db 116 ATTCCACGAGTGCCTCAGATAGGA 93
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RESULT 6
US-10-085-783A-28762/c
; Sequence 28762, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28762
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-28762
Query Match      100.0%; Score 24; DB 18; Length 191;
Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCGCTCAGATAGGA 24
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Db 116 ATTCCACGAGTGCCTCAGATAGGA 93

RESULT 7
US-10-242-535A-54131/c
; Sequence 54131, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54131
; LENGTH: 370
; TYPE: DNA
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Best Local Similarity 79.2%; Pred. No. 0.11;
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Db 313 ATTCCACGAGTGCCTCAGATAGGA 290

RESULT 8
US-10-085-783A-54131/c
; Sequence 54131, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
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; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54131
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-54131
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Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCGCTCAGATAGGA 24
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Db 313 ATTCCACGAGTGCCTCAGATAGGA 290

RESULT 9
US-10-242-535A-31372/c
; Sequence 31372, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31372
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-31372
Query Match      100.0%; Score 24; DB 17; Length 468;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGCGCTCAGATAGGA 24
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Db 409 ATTCCACGAGTGCCTCAGATAGGA 386

RESULT 10
US-10-085-783A-31372/c
; Sequence 31372, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
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; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31372
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Human
; US-10-085-783A-31372

Query Match      100.0%; Score 24; DB 18; Length 468;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGGCGCUCAGAUAGGA 24
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Db      409 ATTCACCAGTGCCTCAGATAGGA 386

RESULT 11
US-10-437-931-1/c
; Sequence 1, Application US/10437931
; Publication No. US20030215868A1
; GENERAL INFORMATION:
; APPLICANT: Seeman, Philip
; APPLICANT: No. US20030215868A1al, Gabriela
; APPLICANT: Tallierico, Teresa
; TITLE OF INVENTION: Method of Detecting Schizophrenia
; FILE REFERENCE: 13459-1
; CURRENT APPLICATION NUMBER: US/10/437,931
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: UK 0211212.6
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-437-931-1

Query Match      100.0%; Score 24; DB 17; Length 972;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGGCGCUCAGAUAGGA 24
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Db      265 ATTCACCAGTGCCTCAGATAGGA 242

RESULT 12
US-09-765-205-5/c
; Sequence 5, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0

; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31372
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Human
; US-10-085-783A-31372

Query Match      100.0%; Score 24; DB 18; Length 468;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGGCGCUCAGAUAGGA 24
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Db      409 ATTCACCAGTGCCTCAGATAGGA 386

RESULT 11
US-10-437-931-1/c
; Sequence 1, Application US/10437931
; Publication No. US20030215868A1
; GENERAL INFORMATION:
; APPLICANT: Seeman, Philip
; APPLICANT: No. US20030215868A1al, Gabriela
; APPLICANT: Tallierico, Teresa
; TITLE OF INVENTION: Method of Detecting Schizophrenia
; FILE REFERENCE: 13459-1
; CURRENT APPLICATION NUMBER: US/10/437,931
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: UK 0211212.6
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-437-931-1

Query Match      100.0%; Score 24; DB 17; Length 972;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGGCGCUCAGAUAGGA 24
       |:|||||:|||||:|||||:|||||
Db      265 ATTCACCAGTGCCTCAGATAGGA 242

RESULT 12
US-09-765-205-5/c
; Sequence 5, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
; US-09-765-205-5

Query Match      100.0%; Score 24; DB 9; Length 1610;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGGCGCUCAGAUAGGA 24
       |:|||||:|||||:|||||:|||||
Db      1518 ATTCACCAGTGCCTCAGATAGGA 1495

RESULT 13
US-10-347-669-5/c
; Sequence 5, Application US/10347669
; Publication No. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
; US-10-347-669-5

Query Match      100.0%; Score 24; DB 21; Length 1610;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGGCGCUCAGAUAGGA 24
       |:|||||:|||||:|||||:|||||
Db      1518 ATTCACCAGTGCCTCAGATAGGA 1495

RESULT 14
US-10-439-388-62/c
; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,388
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-439-388-62

Query Match      100.0%; Score 24; DB 17; Length 1785;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGGCGCUCAGAUAGGA 24
       |:|||||:|||||:|||||:|||||
Db      1078 ATTCACCAGTGCCTCAGATAGGA 1055
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:02:47 ; Search time 483.108 Seconds
(without alignments)
334.933 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
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- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	19.2	76.8	270	9	US-09-294-093B-149
C 2	19.2	76.8	597	20	US-10-425-115-117468
C 3	19.2	76.8	40304	11	US-09-997-722-280
C 4	19.2	76.8	86574	19	US-10-775-169-173
5	18.6	74.4	391	9	US-09-960-352-8669
6	18.6	74.4	402	9	US-09-960-352-11019
7	18.6	74.4	422	9	US-09-960-352-5872

C 8	18.6	74.4	1830121	17	US-10-329-670-1	Sequence 1, Appli
C 9	18.6	74.4	1830121	20	US-10-158-865-1	Sequence 1, Appli
C 10	18.6	74.4	1830121	22	US-10-981-687-1	Sequence 1, Appli
C 11	18.4	73.6	564	22	US-10-972-079-58889	Sequence 58889, A
C 12	18.4	73.6	8473	9	US-09-851-682A-2	Sequence 2, Appli
C 13	18	72.0	601	22	US-10-893-315-332	Sequence 332, App
C 14	18	72.0	601	22	US-10-893-315-1543	Sequence 1543, Ap
C 15	18	72.0	117231	22	US-10-893-315-129	Sequence 129, App
C 16	18	72.0	119226	22	US-10-893-315-159	Sequence 159, App
C 17	18	72.0	119313	22	US-10-893-315-164	Sequence 164, App
C 18	18	72.0	149382	21	US-10-741-600-17661	Sequence 17661, A
C 19	17.8	71.2	2369	20	US-10-739-930-4146	Sequence 4146, Ap
C 20	17.6	70.4	460	10	US-09-918-995-9075	Sequence 9075, Ap
C 21	17.6	70.4	528	19	US-10-767-701-27619	Sequence 27619, A
C 22	17.6	70.4	544	13	US-10-027-632-90568	Sequence 90568, A
C 23	17.6	70.4	544	13	US-10-027-632-304306	Sequence 304306, A
C 24	17.6	70.4	544	17	US-10-027-632-90568	Sequence 90568, A
C 25	17.6	70.4	544	17	US-10-027-632-304306	Sequence 304306, A
C 26	17.6	70.4	605	18	US-10-424-599-65155	Sequence 65155, A
C 27	17.6	70.4	1441	20	US-10-723-860-7987	Sequence 7987, Ap
C 28	17.6	70.4	1994	9	US-09-864-761-4614	Sequence 4614, Ap
C 29	17.6	70.4	2562	14	US-10-237-271-8	Sequence 8, Appli
C 30	17.6	70.4	2562	16	US-10-354-358-13	Sequence 13, Appli
C 31	17.6	70.4	2562	21	US-10-772-636-43	Sequence 43, Appli
C 32	17.6	70.4	2712	17	US-10-104-047-337	Sequence 337, App
C 33	17.6	70.4	2756	17	US-10-388-360-362	Sequence 362, App
C 34	17.6	70.4	2756	21	US-10-956-157-904	Sequence 904, App
C 35	17.6	70.4	3135	19	US-10-437-963-9258	Sequence 9258, Ap
C 36	17.6	70.4	19696	10	US-09-764-891-9327	Sequence 9327, Ap
C 37	17.6	70.4	19696	14	US-10-091-572-874	Sequence 874, App
C 38	17.4	69.6	1152	13	US-10-027-632-118560	Sequence 118560, A
C 39	17.4	69.6	1152	13	US-10-027-632-123821	Sequence 123821, A
C 40	17.4	69.6	1152	13	US-10-027-632-123822	Sequence 123822, A
C 41	17.4	69.6	1152	13	US-10-027-632-123823	Sequence 123823, A
C 42	17.4	69.6	1152	17	US-10-027-632-118560	Sequence 118560, A
C 43	17.4	69.6	1152	17	US-10-027-632-123821	Sequence 123821, A
C 44	17.4	69.6	1152	17	US-10-027-632-123822	Sequence 123822, A
C 45	17.4	69.6	1152	17	US-10-027-632-123823	Sequence 123823, A

ALIGNMENTS

RESULT 1

US-09-294-093B-149/c
; Sequence 149, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700342237H1
US-09-294-093B-149

Query Match 76.8%; Score 19.2; DB 9; Length 270;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 15; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUCCAGAUAGCCC 25

Db 46 ATCTTCAGCATTCAGATATGACC 23
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RESULT 2
US-10-425-115-117468/c
; Sequence 117468, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 117468
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_38619C.1
US-10-425-115-117468
Query Match 76.8%; Score 19.2; DB 20; Length 597;
Best Local Similarity 62.5%; Pred. No. 49;
Matches 15; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUUCAGAUAGCCCC 25
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Db 287 ATCTTCAGCATTCAGATATGACC 264
RESULT 3
US-09-997-722-280/c
; Sequence 280, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 280
; LENGTH: 40304
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14527)..(15049)
; OTHER INFORMATION: "n" at position 14527 through 15049 can be any base.
US-09-997-722-280
Query Match 76.8%; Score 19.2; DB 11; Length 40304;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUUCAGAUAGCCCC 25
| : : | | | | : : | | | | : : | | |
Db 37678 AACTTGAGGATGCCAGATATGCC 37655
RESULT 4

US-10-775-169-173/c
; Sequence 173, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dornier, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 86574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-173
Query Match 76.8%; Score 19.2; DB 19; Length 86574;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUUCAGAUAGCCCC 25
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Db 36754 AACTTGAGGATGCCAGATATGCC 36731
RESULT 5
US-09-960-352-8669
; Sequence 8669, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8669
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 37-LIB34-021-Q1-E1-B2
US-09-960-352-8669
Query Match 74.4%; Score 18.6; DB 9; Length 391;
Best Local Similarity 64.0%; Pred. No. 92;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAACUUCAGGAUUCAGAUAGCCCC 25
| : : | | | | : : | | | | : : | | |
Db 63 CAATTCGAGTCCAGATGTCGCC 87
RESULT 6
US-09-960-352-11019
; Sequence 11019, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C

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1 // SEQ ID NO 1
2 // LENGTH: 1830121
3 // TYPE: DNA
4 // ORGANISM: Haemophilus influenzae
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8 // OTHER INFORMATION: n equals a, t, g or c
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73 // FEATURE:

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/ NAME/KEY: misc feature
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/ NAME/KEY: misc feature
/ LOCATION: (119924)..(119924)
/ OTHER INFORMATION: n equals a, t, g or c
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/ NAME/KEY: misc feature
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/ OTHER INFORMATION: n equals a, t, g or c
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/ NAME/KEY: misc feature
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/ LOCATION: (152500)..(152500)
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Query Match 74.4%; Score 18.6; DB 17; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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QY 1 CAACTTCAGGATGCCCTTTATGCC 1071754
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Db 1071778 CAACTTCAGGATGCCCTTTATGCC 1071754
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RESULT 9
US-10-158-865-1/c
; Sequence 1, Application US/10158865
; Publication No. US20040203093A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragm
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P2C1D1
; CURRENT APPLICATION NUMBER: US/10/158,865
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/557,884
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 08/476,102
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Haemophilus influenzae
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Best Local Similarity 64.0%; Pred. No. 2.le+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUUGCCC 25
Db 1071778 CAACUUCAGGAUCCAGGAUUGCCC 1071754
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RESULT 10
US-10-981-687-1/c
/ Sequence 1, Application US/10981687
/ Publication No. US20050131222A1
/ GENERAL INFORMATION:
/ APPLICANT: Fleischmann et al.
/ TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
/ FILE REFERENCE: PB186P2CID12
/ CURRENT APPLICATION NUMBER: US/10/981,687
/ CURRENT FILING DATE: 2004-11-05
/ PRIOR APPLICATION NUMBER: US 10/159,865
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US 09/557,884
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: US 08/476,102
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: US 08/426,787
/ PRIOR FILING DATE: 1995-04-21
/ NUMBER OF SEQ ID NOS: 1
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1830121
/ TYPE: DNA
/ ORGANISM: Haemophilus Influenzae
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Query Match 74.4%; Score 18.6; DB 22; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db 1071778 CAACUCCAGGAUCCAGGAUAGCCC 1071754

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US-10-972-079-58889
; Sequence 58889, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 58889
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Chicken 19866894316535_1
US-10-972-079-58889

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Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 6 UCAGGAUCCAGAUAGCCC 25
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Db 318 TCAGGTTTCAGATATGCC 337

RESULT 12
US-09-851-682A-2/c
; Sequence 2, Application US/09851682A
; Patent No. US20020091248A1
; GENERAL INFORMATION:

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; APPLICANT: Adams, Arwen E.
; APPLICANT: Chiu, Choi Ying
; APPLICANT: Duhl, David
; APPLICANT: Gorman, Susan W.
; APPLICANT: Leng, Song
; APPLICANT: Sheffield, Val
; APPLICANT: Welch, Juliet
; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
; FILE REFERENCE: 200130.442
; CURRENT APPLICATION NUMBER: US/09/851,682A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US/09/172,422
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 8473
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-851-682A-2

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Best Local Similarity 65.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      2 AACUUCAGGAUCCAGAUU 21
DB      1595 AACCTCAGGATTACAGATAT 1576

RESULT 13
US-10-893-315-332/c
; Sequence 332, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-10-893-315-332

Query Match      72.0%; Score 18; DB 22; Length 601;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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DB      521 CAACCTCAGGATTCAGCA 504

RESULT 14
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; Sequence 1543, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
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; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
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; ORGANISM: Human
US-10-893-315-1543

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DB      521 CAACCTCAGGATTCAGCA 504

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; Sequence 129, Application US/10893315
; Publication No. US20050147987A1
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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 117231
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; OTHER INFORMATION: n = A,T,C or G
US-10-893-315-129

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DB      4257 CAACCTCAGGATTCAGCA 4240

Search completed: July 30, 2005, 15:29:44
Job time : 490.108 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:02:47 ; Search time 483.108 Seconds
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Title: US-09-544-776-3

Perfect score: 25
Sequence: 1 cuggaagcuggaucacacccuug 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	25	100.0	75	9	US-09-758-140-7
C 3	25	100.0	75	9	US-09-772-599A-7
C 4	25	100.0	75	9	US-09-772-599A-23
C 5	25	100.0	90	9	US-09-772-599A-25
C 6	25	100.0	105	9	US-09-772-599A-27
C 7	25	100.0	120	9	US-09-758-140-17

C 8	25	100.0	120	9	US-09-772-599A-17	Sequence 17, Appl
C 9	25	100.0	198	9	US-09-758-140-19	Sequence 19, Appl
C 10	25	100.0	198	9	US-09-772-599A-19	Sequence 19, Appl
C 11	25	100.0	198	9	US-09-772-599A-21	Sequence 21, Appl
C 12	25	100.0	198	9	US-10-327-213-10	Sequence 10, Appl
C 13	25	100.0	261	18	US-10-660-946-9	Sequence 9, Appl
C 14	25	100.0	600	21	US-10-956-157-9764	Sequence 9764, Ap
C 15	25	100.0	639	9	US-09-880-107-3484	Sequence 3484, Ap
C 16	25	100.0	668	17	US-10-264-237-163	Sequence 163, App
C 17	25	100.0	799	18	US-10-660-946-2	Sequence 2, Appl
C 18	25	100.0	994	11	US-09-978-360A-110	Sequence 110, App
C 19	25	100.0	1122	9	US-09-789-386-5	Sequence 5, Appl
C 20	25	100.0	1160	14	US-10-175-523-156	Sequence 156, App
C 21	25	100.0	1400	21	US-10-956-157-9762	Sequence 9762, Ap
C 22	25	100.0	1400	21	US-10-956-157-9763	Sequence 9763, Ap
C 23	25	100.0	1400	21	US-10-956-157-9765	Sequence 9765, Ap
C 24	25	100.0	1400	21	US-10-956-157-9766	Sequence 9766, Ap
C 25	25	100.0	1400	21	US-10-956-157-9767	Sequence 9767, Ap
C 26	25	100.0	1514	9	US-09-823-245A-349	Sequence 349, App
C 27	25	100.0	1609	21	US-10-956-157-4527	Sequence 4527, Ap
C 28	25	100.0	1610	9	US-09-765-205-5	Sequence 5, Appl
C 29	25	100.0	1610	21	US-10-347-669-5	Sequence 5, Appl
C 30	25	100.0	1785	17	US-10-439-388-62	Sequence 62, Appl
C 31	25	100.0	1785	21	US-10-956-157-1705	Sequence 1705, Ap
C 32	25	100.0	1798	19	US-10-466-258-10	Sequence 10, Appl
C 33	25	100.0	1798	22	US-10-466-391A-10	Sequence 10, Appl
C 34	25	100.0	1980	17	US-10-220-891-22	Sequence 22, Appl
C 35	25	100.0	2050	21	US-10-956-157-4530	Sequence 4530, Ap
C 36	25	100.0	2052	19	US-10-466-258-3	Sequence 3, Appl
C 37	25	100.0	2052	22	US-10-466-391A-3	Sequence 3, Appl
C 38	25	100.0	2235	21	US-10-956-157-4531	Sequence 4531, Ap
C 39	25	100.0	2235	14	US-10-060-036-54	Sequence 54, Appl
C 40	25	100.0	2610	18	US-10-641-643-382	Sequence 382, App
C 41	25	100.0	2803	21	US-10-956-157-4529	Sequence 4529, App
C 42	25	100.0	3478	21	US-10-956-157-4528	Sequence 4528, Ap
C 43	25	100.0	3579	9	US-09-789-386-1	Sequence 1, Appl
C 44	25	100.0	3579	9	US-09-893-348-22	Sequence 22, Appl
C 45	25	100.0	3579	18	US-10-267-502-212	Sequence 212, App

ALIGNMENTS

RESULT 1

US-10-956-157-169389/c
; Sequence 169389, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-169389

Query Match 100.0%; Score 25; DB 21; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.034; Indels 0; Gaps 0;
Matches 18; Conservative 7; Mismatches 0;

Qy 1 CUGGAAGCUGGAUCACACCCUUG 25

Db 25 CTGGATAGCTTGGATCATCACCCCTTG 1

RESULT 2

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US-09-758-140-7/c
; Sequence 7, Application US/09758140
; Patent No. US20020012965A1
GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA encoding
; OTHER INFORMATION: receptor binding inhibitor Pep1
US-09-758-140-7
Query Match          100.0%; Score 25; DB 9; Length 75;
Best Local Similarity 72.08; pred.No. 0.039; Indels 0; Gaps 0;
Matches 18; Conservative 7; Mismatches 0;

Qy      1 CUGGAUAGCUUGGUAUCACACCCUUG 25
Db      36 CTGGATAGCTTGGATCACAACCCTTG 12
       |:|::||::||::||::||::||::||
RESULT 3
US-09-972-599A-7/c
; Sequence 7, Application US/09972599A
; Patent No. US20020077295A1
GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA encoding
; OTHER INFORMATION: receptor binding inhibitor Pep 1
US-09-972-599A-7
Query Match          100.0%; Score 25; DB 9; Length 75;
Best Local Similarity 72.08; pred.No. 0.039; Indels 0; Gaps 0;
Matches 18; Conservative 7; Mismatches 0;

Qy      1 CUGGAUAGCUUGGUAUCACACCCUUG 25
Db      36 CTGGATAGCTTGGATCACAACCCTTG 12

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Query Match 100.0%; Score 25; DB 9; Length 90;
Best Local Similarity 72.0%; Pred. No. 0.04;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
| : | | : | | : | | : | | : |
Db 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 6

```

US-09-972-599A-27/c
; Sequence 27, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1089
; OTHER INFORMATION: of human No. US20020077295A1oa
US-09-972-599A-27

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Query Match 100.0%; Score 25; DB 9; Length 105;
Best Local Similarity 72.0%; Pred. No. 0.041;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGUAUCACACCCUUG 25
| : | : | : | : | : | : | : | :
Dd 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 7

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RESOL: 7
US-09-758-140-17/c
; Sequence 17, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA encoding

```

OTHER INFORMATION: receptor binding inhibitor Pep2-41
US-09-758-140-17

Query Match 100.0%; Score 25; DB 9; Length 120;
Best Local Similarity 72.0%; Pred. No. 0.042;
Matches 18; Conservative 7; Mismatches 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
 | : | : | : | : | : | : | : | : | : |
pB 33 CTGGATAGCTTGGATCACACCCTTG 9

RESULT 8

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US-09-972-599A-17/c
; Sequence 17, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA encoding
; OTHER INFORMATION: receptor binding inhibitor Pep2-41
US-09-972-599A-17

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Query Match 100.0%; Score 25; DB 9; Length 120;
Best Local Similarity 72.0%; Pred. No. 0.042;
Matches 18: Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Oy

1 CUGGAUAGCUUGGAUCACACCCTTUG 25
| : | | : | : | : | : | : |
Dd 33 CTGGATAGCTTTGATCACACCCCTTG 9

PRECIT.T 9

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RESOUR 3
US-09-758-140-19/c
; Sequence 19, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020012965A1o gene
US-09-758-140-19

Query Match      100.0%; Score 25; DB 9; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 36 CTGGATAGCTTGGATCACACCCCTTG 12

RESULT 10
US-09-972-599A-19/c
; Sequence 19, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020077295A1o gene
US-09-972-599A-19

Query Match      100.0%; Score 25; DB 9; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 36 CTGGATAGCTTGGATCACACCCCTTG 12

RESULT 11
US-09-972-599A-21/c
; Sequence 21, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 57
; PRIOR FILING DATE: 2000-09-29
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; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1120
; OTHER INFORMATION: of human No. US20020077295A1oA
US-09-972-599A-21

Query Match      100.0%; Score 25; DB 9; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 12
US-10-327-213-10/c
; Sequence 10, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-327-213-10

Query Match      100.0%; Score 25; DB 19; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 13
US-10-660-946-9/c
; Sequence 9, Application US/10660946
; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Au-Young, Janice
; Goli, Surya K.
; Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/660,946
;; FILING DATE: 12-Sep-2003
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/228,213A
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 08/700,607
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0114 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 261 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; IMMEDIATE SOURCE:
;; LIBRARY: SPLNPET01
;; CLONE: 28742
;; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-660-946-9

Query Match 100.0%; Score 25; DB 18; Length 261;
Best Local Similarity 72.0%; Pred. No. 0.046;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUACACCCUUG 25
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Db 124 CTGGATAGCTTGGATCACACCCCTTG 100

RESULT 14

US-10-956-157-9764/c
;; Sequence 9764, Application US/10956157
;; Publication No. US20050118625A1
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Mounts, William
;; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
;; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;; FILE REFERENCE: 031896-043000 (AM 101081)
;; CURRENT APPLICATION NUMBER: US/10/956,157
;; CURRENT FILING DATE: 2004-10-04
;; NUMBER OF SEQ ID NOS: 319805
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 9764
;; LENGTH: 600
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-956-157-9764

Query Match 100.0%; Score 25; DB 21; Length 600;
Best Local Similarity 72.0%; Pred. No. 0.051;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUACACCCUUG 25
|:|||||:|||||:|||||:|
Db 216 CTGGATAGCTTGGATCACACCCCTTG 192

RESULT 15

US-09-880-107-3484/c
;; Sequence 3484, Application US/09880107

;; Patent No. US20020142981A1
;; GENERAL INFORMATION:
;; APPLICANT: Horne, Darci T.
;; APPLICANT: Vockley, Joseph G.
;; APPLICANT: Scherf, Uwe
;; APPLICANT: Gene Logic, Inc.
;; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;; FILE REFERENCE: 44921-5028-WO
;; CURRENT APPLICATION NUMBER: US/09/880,107
;; CURRENT FILING DATE: 2001-06-14
;; PRIOR APPLICATION NUMBER: US 60/211,379
;; PRIOR FILING DATE: 2000-06-14
;; PRIOR APPLICATION NUMBER: US 60/237,054
;; PRIOR FILING DATE: 2000-10-02
;; NUMBER OF SEQ ID NOS: 3950
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3484
;; LENGTH: 639
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US20020142981A1 W27023
;; NAME/KEY: unsure
;; LOCATION: (1)..(639)
;; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3484

Query Match 100.0%; Score 25; DB 9; Length 639;
Best Local Similarity 72.0%; Pred. No. 0.052;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUACACCCUUG 25
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OM nucleic - nucleic search, using sw model

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Title: US-09-544-776-1

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Post-processing: Minimum Match 0%

Maximum Match 100%

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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2231	99.6	2235	14	US-10-060-036-54
2	2191	97.8	2226	21	US-10-060-036-54
3	1908	85.2	2050	21	US-10-060-036-54
4	1892.8	84.5	2052	19	US-10-060-036-54
5	1892.8	84.5	2052	22	US-10-060-036-54
6	1607.4	71.8	1610	9	US-09-765-205-5
7	1607.4	71.8	1610	21	US-10-347-669-5

8	1488.8	66.5	1798	19	US-10-466-258-10	Sequence 10, Appl
9	1488.8	66.5	1798	22	US-10-466-258-10	Sequence 10, Appl
10	1473.4	65.8	1514	9	US-09-823-245A-349	Sequence 349, Appl
11	1409	62.9	4632	14	US-10-060-036-53	Sequence 53, Appl
12	1370	61.2	1609	21	US-10-060-036-53	Sequence 4527, Ap
13	1369	61.1	1400	21	US-10-060-036-53	Sequence 4527, Ap
14	1369	61.1	1400	21	US-10-060-036-53	Sequence 4527, Ap
15	1359.2	60.7	1785	17	US-10-439-388-62	Sequence 62, Appl
16	1359.2	60.7	1785	21	US-10-439-388-62	Sequence 62, Appl
17	1299	58.0	1400	21	US-10-060-036-53	Sequence 1705, Ap
18	1299	58.0	1400	21	US-10-060-036-53	Sequence 1705, Ap
19	1258	56.2	1400	21	US-10-060-036-53	Sequence 1705, Ap
20	1122	50.1	1122	9	US-09-789-386-5	Sequence 5, Appli
21	1097.6	49.0	2610	18	US-10-641-643-382	Sequence 382, App
22	1057	47.2	2782	15	US-10-205-194-165	Sequence 165, App
23	1010.2	45.1	4710	10	US-09-764-891-7385	Sequence 7385, Ap
24	910	40.6	1160	14	US-10-175-523-156	Sequence 156, App
25	907	40.5	4053	9	US-09-758-140-5	Sequence 5, Appli
26	907	40.5	4053	9	US-09-758-140-5	Sequence 5, Appli
27	907	40.5	4053	19	US-10-717-597-310	Sequence 110, App
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33	751.8	33.6	4684	9	US-09-833-348-17	Sequence 4528, Ap
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36	610.4	27.2	3413	13	US-10-001-843-61	Sequence 2, Appli
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43	565.4	25.2	3579	19	US-10-327-213-8	Sequence 8, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 54, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-54

Query Match 99.6%; Score 2231; DB 14; Length 2235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 4531, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4531
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4531

Query Match 97.8%; Score 2191; DB 21; Length 2226;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2218; Conservative 0; Mismatches 0; Indels 7; Gaps 2;

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Qy 2108 ATTATTAATTAACAAATGAAGATTTATACCAATTTGTTTAAAGCTGATGAACTAAATC 2167
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Qy 2168 TGTGGAATGCAATGTAACCTGTAAGCAAGAAATGATCAATAAAGCTTATAGACTT 2221
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RESULT 4

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US-10-466-258-3
; Sequence 3, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2052
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1188)
US-10-466-258-3

Query Match      84.5%; Score 1892.8; DB 19; Length 2052;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2044; Conservative 0; Mismatches 2; Indels 110; Gaps 4;

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Db 181 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Qy 312 CCAGCCATGGAAGACCTTGAACCAAGTCTCTCTGCTCTGCTCTGGAACAGCCACCCCG 371
Db 241 CCAGCCATGGAAGACCTTGAACCAAGTCTCTCTGCTCTGCTCTGGAACAGCCACCCCG 300
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Qy 432 CCAGCCATGGAAGACCTTGAACCAAGTCTCTCTGCTCTGCTCTGGAACAGCCACCCCG 491
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Db 421 GCAGCTTCCGAAATGAGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Qy 552 CTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 611
Db 481 CTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Qy 612 TGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 671
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Qy 672 AGGGGCTCTCTCGCGCTCAGTGTGTTTGAACCTCTCTGCTGAGAGACATTAAGAAGACT 731
Db 601 AGGGGCTCTCTCGCGCTCAGTGTGTTTGAACCTCTCTGCTGAGAGACATTAAGAAGACT 660
Qy 732 GAGTGTGTTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 791
Db 661 GAGTGTGTTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Qy 792 AGCGTAACAGCTTACATTTGGCGCTCTCTCTGCTGAGAGACATTAAGAAGACT 851
Db 721 AGCGTAACAGCTTACATTTGGCGCTCTCTCTGCTGAGAGACATTAAGAAGACT 780
Qy 852 AAGGGTGTGATCAAGCTATCTCAGAAATCAGATGAAGGCCACCCATTCAGGGCAATATCTG 911
Db 781 AAGGGTGTGATCAAGCTATCTCAGAAATCAGATGAAGGCCACCCATTCAGGGCAATATCTG 840
Qy 912 GAATCTGAAGTGTCTATATCTGAGGAGTGTGGTTTCTGAGTGTGAGTGTGAGTGTGAGT 971
Db 841 GAATCTGAAGTGTCTATATCTGAGGAGTGTGGTTTCTGAGTGTGAGTGTGAGTGTGAGT 900
Qy 972 CATGTGACGTGACGATTAAGGAACCTCAGCGCGCTCTCTCTGATGATGATGATGATGAT 1031
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Db 541 TGGACCCGCGCAGCCCGCTCCCGCGCGCCCGCTCCACCCCGCGCGCCCAAGCGC 600
Qy 672 AGGGCTCTCGGGCTCAGTGGTGTGGACCTCTCTGTAAGAGACATTAAGAAGACT 731
Db 601 AGGGCTCTCGGGCTCAGTGGTGTGGACCTCTCTGTAAGAGACATTAAGAAGACT 660
Qy 732 GGAGTGGTGTGGTGGCAGCCTATTCCTGCTGCTTTCATTTGACAGTATTCAGCATTTGG 791
Db 661 GGAGTGGTGTGGTGGCAGCCTATTCCTGCTGCTTTCATTTGACAGTATTCAGCATTTGG 720
Qy 792 AGCGTAACAGCTACATTTGGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATAC 851
Db 721 AGCGTAACAGCTACATTTGGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATAC 780
Qy 852 AAGGGTGTGATCCAAAGTATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTG 911
Db 781 AAGGGTGTGATCCAAAGTATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTG 840
Qy 912 GAATCTGAAGTGTCTATATCTGAGGAGTGGTTCAGAAATCAGTAAATCTGCTCTGGT 971
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Db 1081 CATCAGGCACAGATAGATCATTTATCTAGGACTTCGAAATGAAGATGTTAAAGATGCTATG 1140
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Qy 1626 GTTTGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1685
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Db 1621 TTTAGACGAGATCATACCGGTAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1653
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RESULT 6

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US-09-765-205-5
; Sequence 5, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-09-765-205-5
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Query Match 71.8%; Score 1607.4; DB 9; Length 1610;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CACAGTAGTCCCTCGSCTCAGTCGGCCAGCCCTCTCAGTCCCTCCCAACCCCAACAA 66
Db 1 CACAGTAGTCCCTCGSCTCAGTCGGCCAGCCCTCTCAGTCCCTCCCAACCCCAACAA 60

Qy 67 CCGCCCGCGCTCTGAGACGCGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
Db 61 CCGCCCGCGCTCTGAGACGCGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

Qy 127 ACCCTCAGCCATGGAAGACCTGGAACAGTCTCTCTGCTCTCTCTCTCTCTCTCTCTCT 186
Db 121 ACCCTCAGCCATGGAAGACCTGGAACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

Qy 187 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246
Db 181 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
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Qy 1746 AGGTGATTTGTGACTTTTACTGTTATATTAATTTGCCAATATATAGTAATATATATATAT 1805
Db 1654 ----- 1653

Qy 1806 ATGTATAGTGTTTTACAAAGCTTTAGACCTTTTACCTTCCAGCCACCCCAAGTGTCTGATA 1865
Db 1654 -----ACAAAGCTTTAGACCTTTTACCTTCCAGCCACCCCAAGTGTCTGATA 1699

Qy 1866 TTTTCCAGAGTCAGTCATTGGTTATACATGTAGTTTCCAAAGCACAATAGCTAGAGAAGA 1925
Db 1700 TTTTCCAGAGTCAGTCATTGGTTATACATGTAGTTTCCAAAGCACAATAGCTAGAGAAGA 1759

Qy 1926 AATATTCTTAGGAGCACTACCATCTGTTTCAACATGAATATGCCACACATAGAACTCC 1985
Db 1760 AATATTCTTAGGAGCACTACCATCTGTTTCAACATGAATATGCCACACATAGAACTCC- 1818

Qy 1986 AACAAATCAATTTTATTGTCACAGACTGCTGTTTGTGCAAAATATCAAAATTTGTTATGGA 2045
Db 1819 --CAACATCAATTTTATTGTCACAGACTGCTGTTTGTGCAAAATATCAAAATTTGTTATGGA 1876

Qy 2046 CTGAATCTAATGCTTCCAAATTTGTTTGTGCAAAATATCAAAATTTGTTATGCAAG 2105
Db 1877 CTGAATCTAATGCTTCCAAATTTGTTTGTGCAAAATATCAAAATTTGTTATGCAAG 1936

Qy 2106 AATATTATTAATTAACAAATGAAGATTTATACCATTTGTTTAAAGCTGTACTGAACTAAA 2165
Db 1937 AATATTATTAATTAACAAATGAAGATTTATACCATTTGTTTAAAGCTGTACTGAACTAAA 1996

Qy 2166 TCTGTGGAATGCAATTTGGAATCTTAAAGCAAAAGTATCAATAAGCTTTATAGACTT 2221
Db 1997 TCTGTGGAATGCAATTTGGAATCTTAAAGCAAAAGTATCAATAAGCTTTATAGACTT 2052
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QY 247 AAGAGGAGGAGAAAGAGAGACGAGGACGAAAGACCTCGAAGAGCTGAGGTGCTGGAGA 306
Db 241 AAGAGGAGGAGAAAGAGAGACGAGGACGAAAGACCTCGAAGAGCTGAGGTGCTGGAGA 300
QY 307 GGAAGCCCGCGCGCGGCTGTCCGCGGCCCGCCAGTGTCCACCGCCCTCGCGCGCGCGC 366
Db 301 GGAAGCCCGCGCGCGGCTGTCCGCGGCCCGCCAGTGTCCACCGCCCTCGCGCGCGCGC 360
QY 367 CCTGATGACATTGCGAAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 426
Db 361 CCTGATGACATTGCGAAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 427 CTCGCCCGGTGCGCCCGGAGCGGACGCGTCTTGGGACCCCGAGCCCGGTGTGTCGACCG 486
Db 421 CTCGCCCGGTGCGCCCGGAGCGGACGCGTCTTGGGACCCCGAGCGCGGTGTGTCGACCG 480
QY 487 TGCCCGCGGCATCCCGCGTGTGCTGTGCGCGAGTCTCGCCCTCTCAAGCTCTCGTAGGACG 546
Db 481 TGCCCGCGGCATCCCGCGTGTGCTGTGCGCGAGTCTCGCCCTCTCAAGCTCTCGTAGGACG 540
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QY 607 CCGTGTGACCCCGCCAGCCCGGCTCCCGCGCGCGCCCGCTCCACCCCGCGCGCGCCCA 666
Db 601 CCGTGTGACCCCGCCAGCCCGGCTCCCGCGCGCGCGCCCGCTCCACCCCGCGCGCGCCCA 660
QY 667 AGCGAGGGCTCTCCGGGCTCAGTGGTGTGTGACCTCTGTACTGAGAGACATTAAGA 726
Db 661 AGCGAGGGGCTCTCCGGGCTCAGTGGTGTGTGACCTCTGTACTGAGAGACATTAAGA 720
QY 727 AGACTGGAGTGTGTTGCTGCGACGCTATTCTGCTGCTCTCTGTGACCATCATCTTAGGA 786
Db 721 AGACTGGAGTGTGTTGCTGCGACGCTATTCTGCTGCTCTCTGTGACCATCATCTTAGGA 780
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Db 781 TTGTGAGCGTAACAGCCTACATTTGCTTTGGCGCTCTCTGTGACCATCATCTTAGGA 840
QY 847 TATACAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCAT 906
Db 841 TATACAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCAT 900
QY 907 ATCTGGAATCTGAAGTGTCTATCTGAGGAGTTGGTTTCAGAAGTACAGTAATCTGCTC 966
Db 901 ATCTGGAATCTGAAGTGTCTATCTGAGGAGTTGGTTTCAGAAGTACAGTAATCTGCTC 960
QY 967 TTGTCATGTGAATGCACTGACATAAAGGAACTCAGCGCGCTCTTCTTAGTGTGATTTAG 1026
Db 961 TTGTCATGTGAATGCACTGACATAAAGGAACTCAGCGCGCTCTTCTTAGTGTGATTTAG 1020
QY 1027 TTGATCTCTGAAGTTTGGAGTTGATGTGGTATTTTACCTATGTTGGTCTTGTGTTA 1086
Db 1021 TTGATCTCTGAAGTTTGGAGTTGATGTGGTATTTTACCTATGTTGGTCTTGTGTTA 1080
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Db 1141 AACGGCATCAGGCA CAGATAGATCATTTATCTAGGACTTGGCAATGAAGATGTTAAAGATG 1200
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Db 1201 CTATGGCTAAATCCAGCAAAAATCCCTGGAATTGAAGCGCAAGCTGAATGAAGCGCC 1260
QY 1267 CAAATAATATTAGTAGGAGTTCACTTTTAAAGGGGATATTCAATTTGATTTATACGGGGAGG 1326
Db 1261 CAAATAATATTAGTAGGAGTTCACTTTTAAAGGGGATATTCAATTTGATTTATACGGGGAGG 1320
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QY 1327 GTACGGGAAGAACGAACCTTGACGTTGCGAGTTCGAGTTCACAGATCGTTGTAGATCTTT 1386
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Db 1381 ATTTTATAGCCATGCACTGTTCTGTGAGGAAATTAACCTGTCTTGTACTGCCATGTGTTATC 1440
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QY 1567 CATCTTGGCAGTTGCGAGATGCTGAGCTAGAAAAAATAAAAAA 1615
Db 1561 CATCTTGGCAGTTGCGAGATGCTGAGCTAGAAAAAATAAAAAA 1609

RESULT 7
US-10-347-669-5
; Sequence 5, Application US/10347669
; Publication No. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-10-347-669-5

Query Match 71.8%; Score 1607.4; DB 21; Length 1610;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CACAGTAGTCCCTCGGCTCAGTCGGCCAGCCCTCTCAGTCTCCCAACCCCAACAA 66
Db 1 CACAGTAGTCCCTCGGCTCAGTCGGCCAGCCCTCTCAGTCTCCCAACCCCAACAA 60

QY 67 CCGCCCGCGGCTCTGAGACGCGGCCCGCGCGCGCGCGCGCGCATCATCTCC 126
Db 61 CCGCCCGCGGCTCTGAGACGCGGCCCGCGCGCGCGCGCGCATCATCTCC 120

QY 127 ACCCTCCAGCCATGGAAGACCTGGAACAGTCTCTCTGTGCTCTGTCGAGACCCAC 186
Db 121 ACCCTCCAGCCATGGAAGACCTGGAACAGTCTCTCTGTGCTCTGTCGAGACCCAC 180

QY 187 CCGCGCGCAGCCCGGCTTCAAGTACAGTTCTGAGGAGCGCCGAGGACGAGGAGAG 246
Db 181 CCGCGCGCAGCCCGGCTTCAAGTACAGTTCTGAGGAGCGCCGAGGACGAGGAGAG 240

QY 247 AAGAGGAGGAGGAAGAGGAGGACGAGGACGAAAGACCTTGGAGGAGCTGGAGGTGCTGGAGA 306
Db 241 AAGAGGAGGAGGAAGAGGAGGAGGACGAGGACGAAAGACCTTGGAGGAGCTGGAGGTGCTGGAGA 300

QY 307 GGAAGCCCGCGCGCGGCTGTCCGCGGCCCGCCAGTGTCCACCGCCCTCGCGCGCGCGC 366
Db 301 GGAAGCCCGCGCGCGGCTGTCCGCGGCCCGCCAGTGTCCACCGCCCTCGCGCGCGCGC 360

QY 367 CCCTGATGACATTGCGAAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 426
Db 361 CCCTGATGACATTGCGAAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
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Qy 427 CTCCTCCGTCGCGCCGAGCGGCGAGCCGCTCTGGGACCCGAGCCCGGTGTCGTGACCG 486
Db 421 CTCCTCCGTCGCGCCGAGCGGCGAGCCGCTCTGGGACCCGAGCCCGGTGTCGTGACCG 480
Qy 487 TGCCCGGCGCCATCCCGCTGCTCTGCTCGCGCAGTCTCGCCCTCCAAGCTCCCTCAGGACG 546
Db 481 TGCCCGGCGCCATCCCGCTGCTCTGCTCGCGCAGTCTCGCCCTCCAAGCTCCCTCAGGACG 540
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Qy 607 CCGTGTGAACCCCGCAGCCCGGCTCCGCGCGCGCCCTCCACCGCGCGCGCCCA 666
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Db 661 AGCCGAGGGGCTCTCGGGCTCAGTGGTGTGTGACCTCTCTGTACTGAGAGACATTAAGA 720
Qy 727 AGACTGAGTGGTGTGGTGCCAGCCATATCTGCTGCTCTTCAATGACAGTATTCAGCA 786
Db 721 AGACTGAGTGGTGTGGTGCCAGCCATATCTGCTGCTCTTCAATGACAGTATTCAGCA 780
Qy 787 TTGTGAGGTGAACGCTACATTCGCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGA 846
Db 781 TTGTGAGGTGAACGCTACATTCGCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGA 840
Qy 847 TATACAGGGGTGATCAAGCTATCAAGAAATCAGATGAAGGCCACCATTCAGGCGAT 906
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Db 901 ATCTGGAATCTGAAAGTGTCTATATCTGAGGAGTGGTTCAGAAGTACAGTAATTCGCTC 960
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Qy 1027 TTGATCTCTGAAGTGTGACGTGTGATGCGGTATTTACCTATGTTGGTCCCTGTTTA 1086
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Db 1501 CTGAGGCACCTGGTGAATAAAAAACCTGTATATTTTACTTTTGTGAGATAGTCTTGCG 1560
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Db 1561 CATCTTGGCAAGTTGCGAGAGATGGTGAGCTAGAAAAAAGAAAAA 1609

RESULT 8
US-10-466-258-10
; Sequence 10, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(814)
US-10-466-258-10

Query Match 66.5%; Score 1488.8; DB 19; Length 1798;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1540; Conservative 0; Mismatches 7; Indels 7; Gaps 4;

Qy 692 GGTGTTGACCTCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAG 751
Db 247 GGTGTTGACCTCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAG 306
Qy 752 CCTATTCCTGCTGCTTTCATTTGACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTC 811
Db 307 CCTATTCCTGCTGCTTTCATTTGACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTC 366
Qy 812 CTGGCCCTCTCTCTGTGACCATCAGCTTTAGATATACAAGGCTGTGATCCAGCTAT 871
Db 367 CTGGCCCTCTCTCTGTGACCATCAGCTTTAGATATACAAGGCTGTGATCCAGCTAT 426
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Qy 932 TGAGGAGTTGGTTCAGAAGTACAGTAATTCGTCTTTGGTCAATGTGAACCTGCACGATAAA 991
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Qy 1171 ATTATCTAGCACTTGCAAAATGAAGTGTAAAGTGTCTATGGCTAAATCCAGCAAAAA 1230
Db 726 ATTATCTAGCACTTGCAAAATGAAGTGTAAAGTGTCTATGGCTAAATCCAGCAAAAA 785
Qy 1231 TCCCTGATTTGAAGCGCAAAAGCTGAATGAAACCGCCCAAAATTAATAGTAGGAGTTCATC 1290
Db 786 TCCCTGATTTGAAGCGCAAAAGCTGAATGAAACCGCCCAAAATTAATAGTAGGAGTTCATC 845
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QY 1291 TTTAAAGGGGATATTCATTTGATTAATACGGGGAGGGTCAGGGAAGAACGAACTTGTGACG 1350
Db 1292 TTTAAAGGGGATATTCATTTGATTAATACGGGGAGGGTCAGGGAAGAACGAACTTGTGACG 905
QY 1351 TTGCAGTCAGTTTTCACAGATCGTTGTTAGATCTTTATTTTAGCCATGCATGTTGTGA 1410
Db 1352 TTGCAGTCAGTTTTCACAGATCGTTGTTAGATCTTTATTTTAGCCATGCATGTTGTGA 965
QY 1411 GGAATAATTTACCTGCTTGTGACCTGATGTTTTCATCATCTTAAAGTATTGTAAGCTGCTAT 1470
Db 1412 GGAATAATTTACCTGCTTGTGACCTGATGTTTTCATCATCTTAAAGTATTGTAAGCTGCTAT 1025
QY 1471 GTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGCTGGAATAA 1526
Db 1472 GTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGCTGGAATAA 1085
QY 1527 AAACCTGTATATTTTACCTGTTTGTGCAGATAGTCTTGGCGCATCTTGGCAAGTTGCAAG 1586
Db 1528 AAACCTGTATATTTTACCTGTTTGTGCAGATAGTCTTGGCGCATCTTGGCAAGTTGCAAG 1145
QY 1587 ATGGTGGAGCTAGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1646
Db 1588 ATGGTGGAGCTAGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1205
QY 1647 CGTGTAGATTTGATGAGATTTTCTGAAATGAAGTGTGTTTGTGACATGATGATGATGATG 1706
Db 1648 CGTGTAGATTTGATGAGATTTTCTGAAATGAAGTGTGTTTGTGACATGATGATGATGATG 1265
QY 1707 AAAGCAGAAATGACAAAGCTGCTTCTTGTGATGTTTCTAGTGTATTTGACATTTTACT 1766
Db 1708 AAAGCAGAAATGACAAAGCTGCTTCTTGTGATGTTTCTAGTGTATTTGACATTTTACT 1325
QY 1767 GTTATATTAATTTGCAATATTAAGTAAATATATGATATATATGATAGTGTTCACAAAGC 1826
Db 1768 GTTATATTAATTTGCAATATTAAGTAAATATATGATATATATGATAGTGTTCACAAAGC 1385
QY 1827 TTAGACCTTTTACCTTCCAGCCACCCACAGTCTTTGATATTTTTCAGAGTCAGTCAATTGGT 1886
Db 1828 TTAGACCTTTTACCTTCCAGCCACCCACAGTCTTTGATATTTTTCAGAGTCAGTCAATTGGT 1445
QY 1887 ATACATGTGTAGTTTCCAAAGCACAATAGCTAGAGAAAGAAATATTTTTCAGAGGCACTACC 1946
Db 1888 ATACATGTGTAGTTTCCAAAGCACAATAGCTAGAGAAAGAAATATTTTTCAGAGGCACTACC 1505
QY 1947 ATCTGTTTTCAACATGAATGCCACACATAGAACTCCAAACATCAATTTTCATTGCA 2006
Db 1948 ATCTGTTTTCAACATGAATGCCACACATAGAACTCCAAACATCAATTTTCATTGCA 1564
QY 2007 CAGACTGACTGTAGTTAATTTTGTACAGAAATCTATGGAATGAATCTTAATGCTTCCAAAA 2066
Db 2008 CAGACTGACTGTAGTTAATTTTGTACAGAAATCTATGGAATGAATCTTAATGCTTCCAAAA 1624
QY 2067 ATGTTGTTTGTGAAATATCAACATTTGATGCAAGAAATTTAATTTACAAATGA 2126
Db 2068 ATGTTGTTTGTGAAATATCAACATTTGATGCAAGAAATTTAATTTACAAATGA 1684
QY 2127 AGATTTATACCAATCTGTTGTTTAAAGCTGTACTGAACCTAAATCTGTGGAATGCTGTGAAC 2186
Db 2128 AGATTTATACCAATCTGTTGTTTAAAGCTGTACTGAACCTAAATCTGTGGAATGCTGTGAAC 1744
QY 2187 TGTAAAGCAAGTATCAATAAGCTTATAGACTTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAG 2240
Db 2188 TGTAAAGCAAGTATCAATAAGCTTATAGACTTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAG 1798
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RESULT 9

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US-10-466-391A-10
; Sequence 10, Application US/10466391A
; Publication No. US20040146953A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
```

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; CURRENT APPLICATION NUMBER: US/10/466,391A
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(814)
US-10-466-391A-10
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Query Match      66.5%; Score 1488.8; DB 22; Length 1798;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1540; Conservative 0; Mismatches 7; Indels 7; Gaps 4;

QY 692 GGTGTTTGACCTCTCTGTACTGAGAGACATTTAAGAAGACTGGAGTGGTGTGGTGGCCAG 751
Db 693 GGTGTTTGACCTCTCTGTACTGAGAGACATTTAAGAAGACTGGAGTGGTGTGGTGGCCAG 306
QY 752 CCTATTCTCTGCTCTTTCATTTGACAGATTTTCCAGCATTTGTGAGCGTAAACAGCCTACATTC 811
Db 753 CCTATTCTCTGCTCTTTCATTTGACAGATTTTCCAGCATTTGTGAGCGTAAACAGCCTACATTC 366
QY 812 CTGCCCCCTGCTCTCTGTGACCATCAGCTTTTGGATATATACAAAGGCTGTGATCCAAAGCTAT 871
Db 813 CTGCCCCCTGCTCTCTGTGACCATCAGCTTTTGGATATATACAAAGGCTGTGATCCAAAGCTAT 426
QY 872 CCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTGTCTATATC 931
Db 873 CCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTGTCTATATC 486
QY 932 TGAGAGTGTGGTTTCAAGATGACATTAATCTGCTCTTGGTCTATGTAAGTGTGCAAGATAA 991
Db 933 TGAGAGTGTGGTTTCAAGATGACATTAATCTGCTCTTGGTCTATGTAAGTGTGCAAGATAA 546
QY 992 GGAATCTAGGCGCTCTCTCTTGTAGTATGATGATTTAGTGTGATTTCTGAAAGTGTGCAAGTGT 1051
Db 993 GGAATCTAGGCGCTCTCTCTTGTAGTATGATGATTTAGTGTGATTTCTGAAAGTGTGCAAGTGT 606
QY 1052 GATGTGGGTATTTACCTATATGTTGGTCTGTTTAAAGTCTGACACATCTGATGTTTGGC 1111
Db 1053 GATGTGGGTATTTACCTATATGTTGGTCTGTTTAAAGTCTGACACATCTGATGTTTGGC 666
QY 1112 TCTCATTTTCACT-CTTCAGTGTCTCTGTTTATGTAAGCGCATCAGGACAGATAGATC 1170
Db 1113 TCTCATTTTCACT-CTTCAGTGTCTCTGTTTATGTAAGCGCATCAGGACAGATAGATC 725
QY 1171 ATTATCTAGGACTTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAAA 1230
Db 1172 ATTATCTAGGACTTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAAA 785
QY 1231 TCCCTGGATTAAGCGCAAAAGCTGAATGAAGAAACGCCCCAAAAATAATTAGTAGAGTTTCATC 1290
Db 1232 TCCCTGGATTAAGCGCAAAAGCTGAATGAAGAAACGCCCCAAAAATAATTAGTAGAGTTTCATC 845
QY 1291 TTTAAAGGGGATATTTCAATTTGATTTATAGCGGGAGGGTCAGGGAAGAACCAACCTTGACG 1350
Db 1292 TTTAAAGGGGATATTTCAATTTGATTTATAGCGGGAGGGTCAGGGAAGAACCAACCTTGACG 905
QY 1351 TTGAGTGTGACGTTTTCACAGATCGTTTGTAGATCTTTATTTTGTAGCCATGCACTGTTGTGA 1410
Db 1352 TTGAGTGTGACGTTTTCACAGATCGTTTGTAGATCTTTATTTTGTAGCCATGCACTGTTGTGA 965
QY 1411 GGAATAATTTACCTGCTTGTGACCTGATGTTTTCATCATCTTAAAGTATTGTAAGCTGCTAT 1470
Db 1412 GGAATAATTTACCTGCTTGTGACCTGATGTTTTCATCATCTTAAAGTATTGTAAGCTGCTAT 1025
QY 1471 GTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGCTGGAATAA 1526
Db 1472 GTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGCTGGAATAA 1085
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Db 4234 CTTTACCTTCCAGCCACCCACAGTGTGATATTTTCAGAGTCAGTCATTGGTTATACAT 4293
Qy 1893 GTGTAGTTCGAAGCACATAGCTAGAGAGAAATATTTCTAGAGGACCTACCATCTGT 1952
Db 4294 GTGTAGTTCGAAGCACATAGCTAGAGAGAAATATTTCTAGAGGACCTACCATCTGT 4353
Qy 1953 TTTCAACATGAATGCGCACACACATAGAACTCCAAACACATCAATTTTCATTGACAGACT 2012
Db 4354 TTTCAACATGAATGCGCACACACATAGAACTCCAAACACATCAATTTTCATTGACAGACT 4413
Qy 2013 GACTGTAGTTAATTTGTTCAGAGATCTATGAGCTGAATCTAAATGCTTCCAAAAATGTTG 2072
Db 4414 GACTGTAGTTAATTTGTTCAGAGATCTATGAGCTGAATCTAAATGCTTCCAAAAATGTTG 4473
Qy 2073 TTTGTTGCAAAATCAAAACATTTGTTATGCAAGAAATATTAATTCACAAATGAAGATTT 2132
Db 4474 TTTGTTGCAAAATCAAAACATTTGTTATGCAAGAAATATTAATTCACAAATGAAGATTT 4533
Qy 2133 ATACCATTTGGTTTAAAGCTGTACTGAACATAAATCTGTGGAATGCATTTGTGAACGTAAA 2192
Db 4534 ATACCATTTGGTTTAAAGCTGTACTGAACATAAATCTGTGGAATGCATTTGTGAACGTAAA 4593
Qy 2193 AGCAAGTATCAATAAAGCTTTATAGACTTTAAAAA 2231
Db 4594 AGCAAGTATCAATAAAGCTTTATAGACTTTAAAAA 4632

RESULT 12
US-10-956-157-4527
; Sequence 4527, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4527
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4527

Query Match 61.2%; Score 1370; DB 21; Length 1609;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1467; Conservative 0; Mismatches 0; Indels 67; Gaps 3;

Qy 692 GGTGTTTGACCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGGTGGTGGCAG 751
Db 139 GGTGTTTGACCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGGTGGTGGCAG 198
Qy 752 CCTATTCCTGCTCTTTCATTGACAGTATTCAGCAATTTGTGAGCGTAAACAGCTACATGTC 811
Db 199 CCTATTCCTGCTCTTTCATTGACAGTATTCAGCAATTTGTGAGCGTAAACAGCTACATGTC 258
Qy 812 CTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 871
Db 259 CTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 318
Qy 872 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAATGCTATATC 931
Db 319 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAATGCTATATC 378
Qy 932 TGAGGAGTGGTTTCAAGATACAGTAAATCTGCTCTTGGTCAATGTGAATGCAAGTAAA 991
Db 379 TGAGGAGTGGTTTCAAGATACAGTAAATCTGCTCTTGGTCAATGTGAATGCAAGTAAA 438
Qy 992 GGAACCTAGGGCCCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAGTTGAGTGT 1051

Db 439 GGAACCTAGGGCCCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAGTTTTCAGTGT 498
Qy 1052 GATGTGGGTATTTTACCTATGTTGGTCTCTGTTTAAATGGTCTGACACTACTGATTTTGGC 1111
Db 499 GATGTGGGTATTTTACCTATGTTGGTCTCTGTTTAAATGGTCTGACACTACTGATTTTGGC 558
Qy 1112 TCTCATTTTCACTCTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1171
Db 559 TCTCATTTTCACTCTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 618
Qy 1172 TTTATCTAGGACTTTGCAAAATGAAGATTTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAAT 1231
Db 619 TTTATCTAGGACTTTGCAAAATGAAGATTTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAAT 678
Qy 1232 CCCTGGATTTGAAGCGCAAAAGCTGAATGAATAACCGCCAAATAAATAGTAGAGGATTCATCT 1291
Db 679 CCCTGGATTTGAAGCGCAAAAGCTGAATGAATAACCGCCAAATAAATAGTAGAGGATTCATCT 738
Qy 1292 TTAAGGGGATATTTCAATTTGATTTATACGGGGAGGGTTCAGGGAAGAACGACCTTTGACGT 1351
Db 739 TTAAGGGGATATTTCAATTTGATTTATACGGGGAGGGTTCAGGGA 781
Qy 1352 TGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTTATTTTAGCCATGCACTGTTGTGAG 1411
Db 782 782
Qy 1412 GAAAAATTAACCTGTCTTTCAGTGTGCAATGTTTCATCATCTTAAGTATTTGTAAGCTGCTATG 1471
Db 799 GAAAAATTAACCTGTCTTTCAGTGTGCAATGTTTCATCATCTTAAGTATTTGTAAGCTGCTATG 858
Qy 1472 TATGGATTTTAAACCGTAATCATATCTTTTCCATCTATCTGAGGCACTGGTGGAAATAA 1527
Db 859 TATGGATTTTAAACCGTAATCATATCTTTTCCATCTATCTGAGGCACTGGTGGAAATAA 918
Qy 1528 AAACCTGTATATTTTACTTTGTCAGATAGTCTTGGCGCATCTTGCGCAAGTTTCAGAGA 1587
Db 919 AAACCTGTATATTTTACTTTGTCAGATAGTCTTGGCGCATCTTGCGCAAGTTTCAGAGA 978
Qy 1588 TGTGTGAGCTAGAAAAA 1647
Db 979 TGTGTGAGCTAGAAAAA 1038
Qy 1648 GTGTAGATTGATGCAGATTTTCTGAAATGAATGTTTGTAGACGAGATCATACCGGTA 1707
Db 1039 GTGTAGATTGATGCAGATTTTCTGAAATGAATGTTTGTAGACGAGATCATACCGGTA 1098
Qy 1708 AAGCAGGAATGACAAAGCTTTGCTTTCTGTTAGTCTTAGGTGATTTGTTGACTTTTACTG 1767
Db 1099 AAGCAGGAATGACAAAGCTTTGCTTTCTGTTAGTCTTAGGTGATTTGTTGACTTTTACTG 1158
Qy 1768 TTTATTTAAATTTGCCAATATATAGTAAATATATATATATATATATATATATATATATAT 1827
Db 1159 TTTATTTAAATTTGCCAATATATAGTAAATATATATATATATATATATATATATATATAT 1218
Qy 1828 TAGACCTTTTACCTTCCAGCCACCCCAAGTCTTGTGATTTTTCAGAGTCAGTCAATTTGTTA 1887
Db 1219 TAGACCTTTTACCTTCCAGCCACCCCAAGTCTTGTGATTTTTCAGAGTCAGTCAATTTGTTA 1278
Qy 1888 TAGACGTGTAGTTTCCAAAGCACATAAGCTAGAGAAGAAATATTTCTAGGAGCACTACCA 1947
Db 1279 TACATGTGTAGTTTCCAAAGCACATAAGCTAGAGAAGAAATATTTCTAGGAGCACTACCA 1338
Qy 1948 TCTGTTTTCACATGAAATGCCACACATAGAACTCCAAACACATCAATTTTCAATTCAC 2007
Db 1339 TCTGTTTTCACATGAAATGCCACACATAGAACTCC 1395
Qy 2008 AGACTGACTGTAGTTAAATTTTGTGCAAGATCTATGCACTGAATCTTAATGCTTCCAAAA 2067
Db 1396 AGACTGACTGTAGTTAAATTTTGTGCAAGATCTATGCACTGAATCTTAATGCTTCCAAAA 1455
Qy 2068 TGTGTTTGTGTTTCCAAATATCAACATTTGTTATGCAAGAAATTTATTAATTTACAAATGAA 2127
Db 1456 TGTGTTTGTGTTTCCAAATATCAACATTTGTTATGCAAGAAATTTATTAATTTACAAATGAA 1515

Qy 2128 GATTATACCAATGGTGGTTTAAGCTGTACTGAACCTAAATCTGTGGAATGCATTTGTGAAT 2187
Db 1516 GATTATACCAATGGTGGTTTAAGCTGTACTGAACCTAAATCTGTGGAATGCATTTGTGAAT 1575

Qy 2188 GTAAAGCAAGTAGTCAATAAAGCTTATAGACTT 2221
Db 1576 GTAAAGCAAGTAGTCAATAAAGCTTATAGACTT 1609

RESULT 13
US-10-956-157-9766
; Sequence 9766, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9766
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9766

Query Match 61.1%; Score 1369; DB 21; Length 1400;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1396; Conservative 0; Mismatches 0; Indels 7; Gaps 2;

Qy 823 TCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCTATCCAGAAATCAG 882
Db 1 TCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCTATCCAGAAATCAG 60

Qy 883 ATGAAGGCCACCCATTCTAGGCGCATCTCGAATCTGAAGTTGCTATATCTCAGGAGTTGG 942
Db 61 ATGAAGGCCACCCATTCTAGGCGCATCTCGAATCTGAAGTTGCTATATCTCAGGAGTTGG 120

Qy 943 TTCAGAAGTACAGTAATTCCTCTCTGTGTCATGTGAACCTGCACGCATAAAGGAATCTCAGGC 1002
Db 121 TTCAGAAGTACAGTAATTCCTCTCTGTGTCATGTGAACCTGCACGCATAAAGGAATCTCAGGC 180

Qy 1003 GCCTCTTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGCAGTGTGTATGGGTAT 1062
Db 181 GCCTCTTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGCAGTGTGTATGGGTAT 240

Qy 1063 TTACTATGTTGGTGCCTTGTATATGCTCTGACACTACTGATTTTGGCTCTCATTTTCAC 1122
Db 241 TTACTATGTTGGTGCCTTGTATATGCTCTGACACTACTGATTTTGGCTCTCATTTTCAC 300

Qy 1123 TCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCAAGATAGATCATTTATCTAGGAC 1182
Db 301 TCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCAAGATAGATCATTTATCTAGGAC 360

Qy 1183 TTGCAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAATCCCTGGATTGA 1242
Db 361 TTGCAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAATCCCTGGATTGA 420

Qy 1243 AGCGCAAGCTGAATGAAAAAGCCCAAAATTAATTAGTAGGAGTTTCATCTTTAAAGGGGAT 1302
Db 421 AGCGCAAGCTGAATGAAAAAGCCCAAAATTAATTAGTAGGAGTTTCATCTTTAAAGGGGAT 480

Qy 1303 ATTCATTTGATTATACGGGGGAGGGTTCAGGGAAGAACCAACCTTGCAGCTTGCAGTGCAGT 1362
Db 481 ATTCATTTGATTATACGGGGGAGGGTTCAGGGAAGAACCAACCTTGCAGCTTGCAGTGCAGT 540

Qy 1363 TTCACAGATCGTTGTTAGATCTTTATTTTATGACCATGCACTGTTGTGAGGAAAAATTACC 1422
Db 541 TTCACAGATCGTTGTTAGATCTTTATTTTATGACCATGCACTGTTGTGAGGAAAAATTACC 600

Qy 1423 TGTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTTGAAGCTGCTATGTATGGATTAA 1482
Db 601 TGTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTTGAAGCTGCTATGTATGGATTAA 660

Qy 1483 ACCGTAATCATATCTTTTTC-----CTATCTGAGGCACCTGGTGGGAATAAAAAACCTGTATA 1538
Db 661 ACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACCTGGTGGGAATAAAAAACCTGTATA 720

Qy 1539 TTTTACTTTTGTTCAGATAGTCTTTCGCGCATCTTTCGGAAGTTGCAGAGATGCTGGAGCTA 1598
Db 721 TTTTACTTTTGTTCAGATAGTCTTTCGCGCATCTTTCGGAAGTTGCAGAGATGCTGGAGCTA 780

Qy 1599 GAAAAAAGAAAAAAGCCCTTTTCAGTTTGTGCACCTGTGTATGGTCCGTGTAGATTGA 1658
Db 781 GAAAAAAGAAAAAAGCCCTTTTCAGTTTGTGCACCTGTGTATGGTCCGTGTAGATTGA 840

Qy 1659 TGCAGATTTCTGAAATGAAATGTTTGTGTAGACAGATCATACCGGTAAGACGGAATG 1718
Db 841 TGCAGATTTCTGAAATGAAATGTTTGTGTAGACAGATCATACCGGTAAGACGGAATG 900

Qy 1719 ACBAAGCTTTCCTTTTCTGTTATGTTCTAGGTGATTTGTGACTTTTACTGTTATTAATT 1778
Db 901 ACBAAGCTTTCCTTTTCTGTTATGTTCTAGGTGATTTGTGACTTTTACTGTTATTAATT 960

Qy 1779 GCCAATAATAGTAATATAGATTATATATATATATATATATATATATATATATATATATAT 1838
Db 961 GCCAATAATAGTAATATAGATTATATATATATATATATATATATATATATATATATATAT 1020

Qy 1839 CTTCCAGCCACCCACACAGTCTTGATATTTTCAGAGTCAGTCAGTCATTTGGTTATACATGTGTAG 1898
Db 1021 CTTCCAGCCACCCACACAGTCTTGATATTTTCAGAGTCAGTCAGTCATTTGGTTATACATGTGTAG 1080

Qy 1899 TTCCAAAGCACATAAGCTAGGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAA 1958
Db 1081 TTCCAAAGCACATAAGCTAGGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAA 1140

Qy 1959 CATGAAATGCCACACACATAGAACTCCAAACAACTCAATTTTCATTTGCACAGACTGACTGT 2018
Db 1141 CATGAAATGCCACACACATAGAACTC--CAACATCAATTTTCATTTGCACAGACTGACTGT 1197

Qy 2019 AGTTAAATTTGTGCACAGATCTATGGACTGAATCTAATGCTTCCAAAATGTTGTTGTT 2078
Db 1198 AGTTAAATTTGTGCACAGATCTATGGACTGAATCTAATGCTTCCAAAATGTTGTTGTT 1257

Qy 2079 TGCAAAATATCAAACTGTTATGCAAGAAATTTAATTAACAAATGAAGATTTATATACCA 2138
Db 1258 TGCAAAATATCAAACTGTTATGCAAGAAATTTAATTAACAAATGAAGATTTATATACCA 1317

Qy 2139 TTGTGGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCAATGTGCAACTGTAAAAGCAAA 2198
Db 1318 TTGTGGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCAATGTGCAACTGTAAAAGCAAA 1377

Qy 2199 GTATCAATAAAGCTTATAGACTT 2221
Db 1378 GTATCAATAAAGCTTATAGACTT 1400

RESULT 14
US-10-956-157-4532
; Sequence 4532, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4532

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; LENGTH: 4623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4532

Query Match      61.1%; Score 1369; DB 21; Length 4623;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1466; Conservative 0; Mismatches 0; Indels 67; Gaps 3;

Qy 693 GTTGTGACCTCTCTGTAAGAGAGACATTAAGAGAGCTGGAGTGGTGTGGTGCCAGC 752
Db 3154 GTTGTGACCTCTCTGTAAGAGAGACATTAAGAGAGCTGGAGTGGTGTGGTGCCAGC 3213

Qy 753 CTATTCCTGCTGCTTCATTTGACAGATTTGAGCATTTGAGCGGTAAACAGCCTACATTTGCC 812
Db 3214 CTATTCCTGCTGCTTCATTTGACAGATTTGAGCATTTGAGCGGTAAACAGCCTACATTTGCC 3273

Qy 813 TTGSCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCCAGCTATC 872
Db 3274 TTGSCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCCAGCTATC 3333

Qy 873 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATTTGCTATATCT 932
Db 3334 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATTTGCTATATCT 3393

Qy 933 GAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTTGGTCAATGTGAACCTGCACGATAAAG 992
Db 3394 GAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTTGGTCAATGTGAACCTGCACGATAAAG 3453

Qy 993 GAACTCAGGCGCCTCTCTAGTTGATGATTTAGTGAATCTCTGAAGTTTGCAGTGTG 1052
Db 3454 GAACTCAGGCGCCTCTCTAGTTGATGATTTAGTGAATCTCTGAAGTTTGCAGTGTG 3513

Qy 1053 ATGCGGTATTTACTATGTTGGTGCCTTGTGTAATGCTCTGACATCTGATTTTGGCT 1112
Db 3514 ATGCGGTATTTACTATGTTGGTGCCTTGTGTAATGCTCTGACATCTGATTTTGGCT 3573

Qy 1113 CTCATTTCACTTTCAGTGTTCCTGTTTATTTAATGAACGGCATCAGGCACAGATAGATCAT 1172
Db 3574 CTCATTTCACTTTCAGTGTTCCTGTTTATTTAATGAACGGCATCAGGCACAGATAGATCAT 3633

Qy 1173 TATCTAGACTTGCATTAAGATGATTTAGATGCTATGCTAAATCCAAAGCAAAATC 1232
Db 3634 TATCTAGACTTGCATTAAGATGATTTAGATGCTATGCTAAATCCAAAGCAAAATC 3693

Qy 1233 CCTGATTTGAAGCCGCAAGCTGATGAACGCCCAAAATTAATAGTGGAGTTCATCTT 1292
Db 3694 CCTGATTTGAAGCCGCAAGCTGATGAACGCCCAAAATTAATAGTGGAGTTCATCTT 3753

Qy 1293 TAAAGGGGATATTCATTTGATTTATACGGGGGAGGGTCAGGGAAGAACCAACCTTGACGTT 1352
Db 3754 TAAAGGGGATATTCATTTGATTTATACG----- 3780

Qy 1353 GCAGTGCAATTTACAGATCGTTGTTAGATCTTTATTTTAGCCATGCACTGTTGAGG 1412
Db 3781 -----GATCTTTATTTTAGCCATGCACTGTTGAGG 3813

Qy 1413 AAAAAATTACCTGCTCTGCTGCCATGTTGTTCAATCATCTTAAGTATTTGAAGCTGCTATGT 1472
Db 3814 AAAAAATTACCTGCTCTGCTGCCATGTTGTTCAATCATCTTAAGTATTTGAAGCTGCTATGT 3873

Qy 1473 ATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACCTGGTGGGAATAAAA 1528
Db 3874 ATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACCTGGTGGGAATAAAA 3933

Qy 1529 AACCTGATATTTTACTTTGTCAGATAGTCTTGGCCGATCTTGGCAAGTTGACAGAT 1588
Db 3934 AACCTGATATTTTACTTTGTCAGATAGTCTTGGCCGATCTTGGCAAGTTGACAGAT 3993

Qy 1589 GGTGGAGCTAGAAAAAAGCCCTTTTTCAGTTTGTGCACTGTTGATGTCGCG 1648
Db 3994 GGTGGAGCTAGAAAAAAGCCCTTTTTCAGTTTGTGCACTGTTGATGTCGCG 4053
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Qy 1649 TGTAGATTGATGCGAGATTTTCTGAAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAA 1708
Db 4054 TGTAGATTGATGCGAGATTTTCTGAAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAA 4113

Qy 1709 AGCAGGAATGACAAAGCTTGTCTTTCTGGTATGTTCTTAGTGTATTGTGACTTTTACTGT 1768
Db 4114 AGCAGGAATGACAAAGCTTGTCTTTCTGGTATGTTCTTAGTGTATTGTGACTTTTACTGT 4173

Qy 1769 TATATTAAATTTGCCAATATATAGTAATATATAGTATATATATATATATATATATATATAT 1828
Db 4174 TATATTAAATTTGCCAATATATAGTAATATATAGTATATATATATATATATATATATATAT 4233

Qy 1829 AGACCTTTACCTTCCAGCCACCCACAGTCTTGTATATTTTCAGAGTCAGTCAATTTGGTTAT 1888
Db 4234 AGACCTTTACCTTCCAGCCACCCACAGTCTTGTATATTTTCAGAGTCAGTCAATTTGGTTAT 4293

Qy 1889 ACATGTGTAGTTCCAAAGCACATAAGCTACAAAGAGAAATATATTTCTAGGAGCACTACCAT 1948
Db 4294 ACATGTGTAGTTCCAAAGCACATAAGCTACAAAGAGAAATATATTTCTAGGAGCACTACCAT 4353

Qy 1949 CTGTTTTCAACATGAATGCCACACATAGAACTCCAAACATCAATTTTCATTTGCACA 2008
Db 4354 CTGTTTTCAACATGAATGCCACACATAGAACTC---CAACATCAATTTTCATTTGCACA 4410

Qy 2009 GACTGACTGTAGTAAATTTTGTTCACAGAACTCTATGGAATCTAATCTTCCAAAAT 2068
Db 4411 GACTGACTGTAGTAAATTTTGTTCACAGAACTCTATGGAATCTAATCTTCCAAAAT 4470

Qy 2069 GTTGTGTTGTTGCAAAATATCAAAATTTGTTATGCAAGAAATTTATTAATTAACAAATGAAG 2128
Db 4471 GTTGTGTTGTTGCAAAATATCAAAATTTGTTATGCAAGAAATTTATTAATTAACAAATGAAG 4530

Qy 2129 ATTTATACCAATCTGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCAATTTGGAATCTG 2188
Db 4531 ATTTATACCAATCTGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCAATTTGGAATCTG 4590

Qy 2189 TAAAGCAAGTATCAATTAAGCTTTATAGACTT 2221
Db 4591 TAAAGCAAGTATCAATTAAGCTTTATAGACTT 4623

RESULT 15
US-10-439-388-62
; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,388
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-439-388-62

Query Match      60.7%; Score 1359.2; DB 17; Length 1785;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 8; Indels 5; Gaps 4;

Qy 692 GGTGTGTGACCTCTCTGTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAG 751
Db 246 GGTGTGTGACCTCTCTGTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAG 305

Qy 752 CCTATTCTCTGCTCTTTCATTTGACGATTTTCAGCATTTGTCAGCGTAAACAGCCTACATTGC 811
Db 306 CCTATTCTCTGCTCTTTCATTTGACGATTTTCAGCATTTGTCAGCGTAAACAGCCTACATTGC 365
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Qy	812	CTTGCCCTGCTCTCTGTGAACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAGCTAT	871
Db	366	CTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTAT	425
Qy	872	CCAGAAATCAGATGAAGGCCACCCATTGAGGATATCTGGAATCTGAAAGTGTCTATATC	931
Db	426	CCAGAAATCAGATGAAGGCCACCCATTGAGGATATCTGGAATCTGAAAGTGTCTATATC	485
Qy	932	TGAGGAGTTGGTTGAGAGTACAGTAATCTGCTCTTGGTCTGATCTGAACTGCACGATAAA	991
Db	486	TGAGGAGTTGGTTGAGAGTACAGTAATCTGCTCTTGGTCTGATCTGAACTGCACGATAAA	545
Qy	992	GGAACTCAGGGGCTCTCTTCTAGTTGATGATTAAGTTGATCTCTGAAAGTTTGCAGTGT	1051
Db	546	GGAACTCAGGGGCTCTCTTCTAGTTGATGATTAAGTTGATCTCTGAAAGTTTGCAGTGT	605
Qy	1052	GATGTGGGTATTACCTATGTTGGTGCCTTGTAAATGAGTCTGATCTGACATCTGATTTGGC	1111
Db	606	GATGTGGGTATTACCTATGTTGGTGCCTTGTAAATGAGTCTGATCTGACATCTGATTTGGC	665
Qy	1112	TCTCATTTTCATCTTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGTCA	1171
Db	666	TCTCATTTTCATCTTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGTCA	725
Qy	1172	TTATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT	1231
Db	726	TTATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT	785
Qy	1232	CCCTGGATGAAGCGCAAGCTGAATGAATAAGCCCAAAAATAATGATGAGGATTCATCT	1291
Db	786	CCCTGGATGAAGCGCAAGCTGAATGAATAAGCCCAAAAATAATGATGAGGATTCATCT	845
Qy	1292	TTAAAGGGGATATCATTTGATTAATACGGGGAGGGTCAGGGAGAAAGAACCTTTGAGCT	1351
Db	846	TTAAAGGGGATATCATTTGATTAATACGGGGAGGGTCAGGGAGAAAGAACCTTTGAGCT	905
Qy	1352	TGCAGTGCAGTTTACAGATCGTTGTTAGATCTTTATTTTATGGCATGCACCTGTTGTGAG	1411
Db	906	TGCAGTGCAGTTTACAGATCGTTGTTAGATCTTTATTTTATGGCATGCACCTGTTGTGAG	965
Qy	1412	GAAAAATTAACCTGCTTGACCTGCCATGTGTTCACTTAAGTATTTGTAAGCTGCTATG	1471
Db	966	GAAAAATTAACCTGCTTGACCTGCCATGTGTTCACTTAAGTATTTGTAAGCTGCTATG	1025
Qy	1472	TATGGATTTAAACCGTAATCATCTTTTCTATCTGAGGCACTGGTGGATAAAAAC	1531
Db	1026	TATGGATTTAAACCGTAATCATCTTTTCTATCTGAGGCACTGGTGGATAAAAAC	1085
Qy	1532	CTGTATATTTTACTTTGTTGAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGT	1591
Db	1086	CTGTATATTTTACTTTGTTGAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGT	1145
Qy	1592	GGAGCTAG-AAAAAATAAGCCCTTTTCAAGTTTGTGCACTGTGTATGTTCCGCTG	1650
Db	1146	GGAGCTAGAAAAAATAAGCCCTTTTCAAGTTTGTGCACTGTGTATGTTCCGCTG	1205
Qy	1651	TAGATTTGATGAGATTTTCTGAAATGAATGTTTGTGTTAGACGAGATCATACCGGTAAG	1710
Db	1206	TAGATTTGATGAGATTTTCTGAAATGAATGTTTGTGTTAGACGAGATCATACCGGTAAG	1265
Qy	1711	CAGGAATGACAAAGCTTCTCTTCTGGTATGTTCTAGGTATTTGTGATCTTTTACTGTTA	1770
Db	1266	CAGGAATGACAAAGCTTCTCTTCTGGTATGTTCTAGGTATTTGTGATCTTTTACTGTTA	1325
Qy	1771	TATTAATTTGCCAATAATAAGTAAATAATAGATATATATATAGTGTTCACAAAGCTTAG	1830
Db	1326	TATTAATTTGCCAATAATAAGTAAATAATAGATATATATATAGTGTTCACAAAGCTTAG	1385
Qy	1831	ACCTTTACCTTCCAGCCACCCACAGTCTGTGATATTTTCAGAGTCAGTCATTTGGTTATAC	1890
Db	1386	ACCTTTACCTTCCAGCCACCCACAGTCTGTGATATTTTCAGAGTCAGTCATTTGGTTATAC	1445

Search completed: August 1, 2005, 20:25:49
Job time : 1318 secs

Qy	1891	ATGTGTAGTTCCAAAGCACATAAGCTAGAGAGAGAAATATTTTCTAGGAGCACTACCATCT	1950
Db	1446	ATGTGTAGTTCCAAAGCACATAAGCTAGAGAGAGAAATATTTTCTAGGAGCACTACCATCT	1505
Qy	1951	GTTTTCAACATGAATGCCACACACATAGAACTCCAACACATCAATTTCAATTCACACAGA	2010
Db	1506	GTTTTCAACATGAATGCCACACACATAGAACTCCAACACATCAATTTCAATTCACACAGA	1565
Qy	2011	CTGACTGTAGTTAATTTTGTCCAGAAATCTATGACTGAATCTAATCTTCCAAAAATGT	2070
Db	1566	CTGACTGTAGTTAATTTTGTCCAGAAATCTATGACTGAATCTAATCTTCCAAAAATGT	1623
Qy	2071	TGTTTGTTCAAAATATCAACATTTGTTATGCAAGAAATTAAT 2112	
Db	1624	TGTTTGTTCAAAATATCAACATTTGTTATGCAAGAAATTTT 1663	

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1525.2	68.1	4822	3	US-09-484-970B-106	Sequence 106, App	
2	1405	62.7	1669	4	US-09-949-016-3253	Sequence 3253, Ap	
3	1097.6	49.0	2610	4	US-09-023-655-382	Sequence 382, App	
4	996.2	44.5	42075	4	US-09-949-016-14995	Sequence 14995, A	
5	682	30.4	799	2	US-08-700-607-2	Sequence 2, Appli	
6	521	23.3	536	4	US-09-621-976-3839	Sequence 3839, Ap	
7	514	22.9	537	4	US-09-513-999C-10680	Sequence 10680, A	
8	482	21.5	508	4	US-09-621-976-3840	Sequence 3840, Ap	
9	381.8	17.0	496	4	US-09-513-999C-11204	Sequence 11204, A	
10	343	15.3	441	4	US-09-513-999C-2227	Sequence 2227, Ap	
11	316.6	14.1	463	4	US-09-621-976-741	Sequence 741, App	
12	316	14.1	454	4	US-09-621-976-740	Sequence 740, App	
13	270.4	12.1	2069	4	US-09-949-016-3309	Sequence 3309, App	
14	270.4	12.1	3202	4	US-09-949-016-1127	Sequence 1127, Ap	
15	263	11.7	301	3	US-09-439-313-279	Sequence 279, App	
16	263	11.7	301	3	US-09-352-616A-279	Sequence 279, App	
17	263	11.7	301	3	US-09-232-149A-279	Sequence 279, App	
18	263	11.7	301	4	US-09-159-812-279	Sequence 279, App	
19	263	11.7	301	4	US-09-636-215-279	Sequence 279, App	
20	263	11.7	301	4	US-09-685-166A-279	Sequence 279, App	
21	263	11.7	301	4	US-09-688-489-279	Sequence 279, App	
22	263	11.7	301	4	US-09-679-426-279	Sequence 279, App	
23	263	11.7	301	4	US-09-759-143-279	Sequence 279, App	
24	263	11.7	301	4	US-09-651-236-279	Sequence 279, App	
25	244.8	10.9	1766	3	US-09-149-476-254	Sequence 254, App	
26	244.8	10.9	2664	3	US-09-149-476-255	Sequence 255, App	
27	236.4	10.6	2262	4	US-09-949-016-2988	Sequence 2988, Ap	

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QY 993 GAACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAAGTTTG 1052
Db 3568 GAACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAAGTTTG 3627
QY 1053 ATGTGGGTATTTACCTATGTTGGTGCCTTTGTTAATGCTCTGACACTACTGATCTTTGGCT 1112
Db 3628 ATGTGGGTATTTACCTATGTTGGTGCCTTTGTTAATGCTCTGACACTACTGATTTGGCT 3687
QY 1113 CTCATTTCACCTCTTCAGTGTGCTCTTATTTATGAACGGGCATCAGGCACAGATAGATCAT 1172
Db 3688 CTCATTTCACCTCTTCAGTGTGCTCTTATTTATGAACGGGCATCAGGCACAGATAGATCAT 3747
QY 1173 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGCTGCTTAAATCAAGCAAAAAATC 1232
Db 3748 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGCTGCTTAAATCAAGCAAAAAATC 3807
QY 1233 CCTGATTTGAACGCAAGCTGAATGAAGAACGCCCAAAATTAATAGTAGGAGTTTCATCTT 1292
Db 3808 CCTGATTTGAACGCAAGCTGAATGAAGAACGCCCAAAATTAATAGTAGGAGTTTCATCTT 3867
QY 1293 TAAAGGGATATTTCAATTTGATTTATACGGGGAGGGTCAGGGAAGAAACGAACCTTGACGTT 1352
Db 3868 TAAAGGGATATTTCAATTTGATTTATACGGGGAGGGTCAGGGAAGAAACGAACCTTGACGTT 3927
QY 1353 GCAGTGCAGTTTCACAGATCGTTGTAGATCTTTATTTTATAGCCATGCACTGTTGTGAGG 1412
Db 3928 GCAGTGCAGTTTCACAGATCGTTGTAGATCTTTATTTTATAGCCATGCACTGTTGTGAGG 3987
QY 1413 AAAAATTAACCTGCTTTGACTGCCATGTTTCATCATCTTAAGTATTGTAAGCTGCTATGT 1472
Db 3988 AAAAATTAACCTGCTTTGACTGCCATGTTTCATCATCTTAAGTATTGTAAGCTGCTATGT 4047
QY 1473 ATGGATTTAAACCGTAATCATATCTTTTCTATCTGAGGCACTGGTGGCAATAAAAAACC 1532
Db 4048 ATGGATTTAAACCGTAATCATATCTTTTCTATCTGAGGCACTGGTGGCAATAAAAAACC 4107
QY 1533 TGTATATTTATTTGTTTGCAGATAGTCTTCCGCACTTTGCGCAATTTGCGATGTTGTCGGT 1592
Db 4108 TGTATATTTATTTGTTTGCAGATAGTCTTCCGCACTTTGCGCAATTTGCGATGTTGTCGGT 4167
QY 1593 GAGCTAG--AAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1650
Db 4168 GAGCTAGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4227
QY 1651 TAGATTGATGAGATTTTCTGAAATGAAATGTTGTTTGTAGACGAGATCATACCGGTAAG 1710
Db 4228 TAGATTGATGAGATTTTCTGAAATGAAATGTTGTTTGTAGACGAGATCATACCGGTAAG 4287
QY 1711 CAGGAATGACAAAGCTTCTTTTCTGATGTTCTGATGTTCTGATGTTCTGATGTTCTGATGTT 1770
Db 4288 CAGGAATGACAAAGCTTCTTTTCTGATGTTCTGATGTTCTGATGTTCTGATGTTCTGATGTT 4347
QY 1771 TATTAATTTGCCATATAGTAATAATAGATTAATATATATATATATATATATATATATATAT 1830
Db 4348 TATTAATTTGCCATATAGTAATAATAGATTAATATATATATATATATATATATATATATATAT 4407
QY 1831 ACCTTTACCTCCAGCCACCCACAGTCTGATATTTTACAGATCAGTCAATTTGGTTATAC 1890
Db 4408 ACCTTTACCTCCAGCCACCCACAGTCTGATATTTTACAGATCAGTCAATTTGGTTATAC 4467
QY 1891 ATGTGTAGTTCCAAAGCACAATAAGCTAGAGAAGAAATATTTTCTAGGAGCACTACCAATCT 1950
Db 4468 ATGTGTAGTTCCAAAGCACAATAAGCTAGAGAAGAAATATTTTCTAGGAGCACTACCAATCT 4527
QY 1951 GTTTTCAACATGAATGCAACACATAGAACTCCAAACATCATATTTTCAATTGACACAGA 2010
Db 4528 GTTTTCAACATGAATGCAACACATAGAACTCCAAACATCATATTTTCAATTGACACAGA 4587
QY 2011 CTGACTGTAGTTAAATTTTGTGACAGAACTTATGGAATCTAATGCTTCCAAAAATGT 2070
Db 4588 CTGACTGTAGTTAAATTTTGTGACAGAACTTATGGAATCTAATGCTTCCAAAAATGT 4647
QY 2071 TGTGTTTGTGCAAAATATCAAACTTTGTTATGCAAGAAATATTAATTAACAAATGAAGAT 2130
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Db 4648 TGTGTTTGTGCAAAATATCAAACTTTGTTATGCAAGAAATTAATTAATTAACAAATGAAGAT 4707
QY 2131 TTATACCAATTTGCTGTTTAAAGCTGACTGAACATAATCTGTGGAATGCAATCTGGAATCTGA 2190
Db 4708 TTATACCAATTTGCTGTTTAAAGCTGACTGAACATAATCTGTGGAATGCAATCTGGAATCTGA 4767
QY 2191 AAAGCAAAATGATCAATAAAGCTTATAGACTTTAAAAAAGGAGGAGGAGGAGGAGGAGGAGG 2240
Db 4768 AAAGCAAAATGATCAATAAAGCTTATAGACTTTAAAAAAGGAGGAGGAGGAGGAGGAGGAGG 4817

RESULT 2
US-09-949-016-3253
; Sequence 3253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3253
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253
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Query Match 62.7%; Score 1405; DB 4; Length 1669;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1419; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 692 GGTGTTGACCTCTCTGCTACTGAGAGACATTAAGAGACTGGAGTGGTGGTGGCCAG 751
Db 247 GGTGTTGACCTCTCTGCTACTGAGAGACATTAAGAGACTGGAGTGGTGGTGGCCAG 306
QY 752 CCTATTCTCTGCTCTTTCATTGACAGTATTCAGCAATTTGAGCGCTAAACAGCTACATTGC 811
Db 307 CCTATTCTCTGCTCTTTCATTGACAGTATTCAGCAATTTGAGCGCTAAACAGCTACATTGC 366
QY 812 CTGCGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTAT 871
Db 367 CTGCGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTAT 426
QY 872 CCAGAAATCAGATGAAGCCACCCATTCAGGCGATATCTGGAATCTGAAAGTTGCTATATC 931
Db 427 CCAGAAATCAGATGAAGCCACCCATTCAGGCGATATCTGGAATCTGAAAGTTGCTATATC 486
QY 932 TGAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCTCATCTGCACTGCACGATAAA 991
Db 487 TGAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCTCATCTGCACTGCACGATAAA 546
QY 992 GGAATCTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGAGTGT 1051
Db 547 GGAATCTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGAGTGT 606
QY 1052 GATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACACTACTGATTTGGC 1111
Db 607 GATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACACTACTGATTTGGC 666
QY 1112 TCTCATTTCTCTCTTCTGAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1171
Db 667 TCTCATTTCTCTCTTCTGAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 726
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QY 1172 TTATCTAGGACTTCAATAGAAATGTTAAAGATGCTATGCTAAATCCAAAGCAAAAT 1231
Db 727 TTATCTAGGACTTCAATAGAAATGTTAAAGATGCTATGCTAAATCCAAAGCAAAAT 786
QY 1232 CCCTGGATTTGAAGCGCAAGCTGAATGAACCGCCAAATAAATAGTAGGAGTTCACT 1291
Db 787 CCCTGGATTTGAAGCGCAAGCTGAATGAACCGCCAAATAAATAGTAGGAGTTCACT 846
QY 1292 TTAAGGGGATATTCATTTGATATTAACGGGGAGGGTCAGGGAAGAACGAACCTTGACGT 1351
Db 847 TTAAGGGGATATTCATTTGATATTAACGGGGAGGGTCAGGGAAGAACGAACCTTGACGT 906
QY 1352 TGCAATGCAAGTTTCAAGATGCTGTTAGATCTTTATTTTATAGCCATGCTGTTGAG 1411
Db 907 TGCAATGCAAGTTTCAAGATGCTGTTAGATCTTTATTTTATAGCCATGCTGTTGAG 966
QY 1412 GAAAAATTTACCTGCTTTCAGCTGCAATGTTTCACTCATCTTAAGATTTAGTAACTGCTATG 1471
Db 967 GAAAAATTTACCTGCTTTCAGCTGCAATGTTTCACTCATCTTAAGATTTAGTAACTGCTATG 1026
QY 1472 TATGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGTTGGAATAA 1527
Db 1027 TATGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGTTGGAATAA 1086
QY 1528 AAACCTGTATATTTTACCTTTGTCAGATAGTCTTGGCGCATCTTGGCAAGTTGCAGAGA 1587
Db 1087 AAACCTGTATATTTTACCTTTGTCAGATAGTCTTGGCGCATCTTGGCAAGTTGCAGAGA 1146
QY 1588 TGTGTGAGCTAGAAAAAAGAAAAAAGCCCTTTTTCAGTTTGTGCTGTTGATGTTCC 1647
Db 1147 TGTGTGAGCTAGAAAAAAGAAAAAAGCCCTTTTTCAGTTTGTGCTGTTGATGTTCC 1206
QY 1648 GTGTGATTTGATGAGATTTTCTGAAATGAAATGTTTGTGATGAGATCATACCGGTA 1707
Db 1207 GTGTGATTTGATGAGATTTTCTGAAATGAAATGTTTGTGATGAGATCATACCGGTA 1266
QY 1708 AAGCAGAAATGACAAAGCTTCTTCTGATGTTTCTGATGTTTCTGATGTTTCTGATGTTTCTG 1767
Db 1267 AAGCAGAAATGACAAAGCTTCTTCTGATGTTTCTGATGTTTCTGATGTTTCTGATGTTTCTG 1326
QY 1768 TTATTTAAATTTGCCAATATAGTAAATATAGATTTATATATAGTGTGTTTTCACAAAGCT 1827
Db 1327 TTATTTAAATTTGCCAATATAGTAAATATAGATTTATATATAGTGTGTTTTCACAAAGCT 1386
QY 1828 TAGACCTTTTACCTTCCAGCCACCCACAGTCTTGTATATTTTTCAGAGTCAGTCAATGTTA 1887
Db 1387 TAGACCTTTTACCTTCCAGCCACCCACAGTCTTGTATATTTTTCAGAGTCAGTCAATGTTA 1446
QY 1888 TACATGTGTAGTTCCAAAGCACAATAGCTAGAGAAATATTTTCTAGAGCACTACCA 1947
Db 1447 TACATGTGTAGTTCCAAAGCACAATAGCTAGAGAAATATTTTCTAGAGCACTACCA 1506
QY 1948 TCTGTTTTCACATGAATGCCACACATAGAACTCAACAACTCAATTTTCAATTCGAC 2007
Db 1507 TCTGTTTTCACATGAATGCCACACATAGAACTCAACAACTCAATTTTCAATTCGAC 1566
QY 2008 AGACTGACTGTAGTTAAATTTTGTTCACAGAACTTATGAGTGAATCTAATGTTTCCAAAAA 2067
Db 1567 AGACTGACTGTAGTTAAATTTTGTTCACAGAACTTATGAGTGAATCTAATGTTTCCAAAAA 1626
QY 2068 TGTGTTTGTGCAATATCAAACTGTTATGATGCAAGAAAT 2110
Db 1627 TGTGTTTGTGCAATATCAAACTGTTATGATGCAAGAAAT 1669

RESULT 3

US-09-023-655-382
; Sequence 382, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT14
; CLONE: 1508778
; US-09-023-655-382

Query Match 49.0%; Score 1097.6; DB 4; Length 2610;

Best Local Similarity 98.4%; Pred. No. 2.6e-255;

Matches 1172; Conservative 0; Mismatches 10; Indels 9; Gaps 6;

QY 692 GGTGTTGACCTCTCTGCTGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCAG 751

Db 1310 GGTGTTGACCTCTCTGCTGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCAG 1369

QY 752 CCTATTCCTGCTCTCTGCTGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCAG 810

Db 1370 CCTATTCCTGCTCTCTGCTGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCAG 1429

QY 811 CCTGCGCCCTCTCTGCTGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCAG 870

Db 1430 CCTGCGCCCTCTCTGCTGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCAG 1489

QY 871 TCCAGAAATCAGATGAAGGCCACCCATTGAGGCAATCTGGAATCTGAAGTGTCTATAT 930

Db 1490 TCCAGAAATCAGATGAAGGCCACCCATTGAGGCAATCTGGAATCTGAAGTGTCTATAT 1549

QY 931 CTGAGGAGTTGGTTCAAGAGTACAGTAATTTCTCTCTTGGTCAATGTAACCTGACGATAA 990

Db 1550 CTGAGGAGTTGGTTCAAGAGTACAGTAATTTCTCTCTTGGTCAATGTAACCTGACGATAA 1609

QY 991 AGGAATCAGCGCCCTCTCTGAGTGTGATTTAGTGTCTCTGAACTTTGCACTGT 1050

Db 1610 AGGAATCAGCGCCCTCTCTGAGTGTGATTTAGTGTCTCTGAACTTTGCACTGT 1669

QY 1051 TGATGTGGGTATTTTACCTATGTTGGTCCCTGTTGTTAATGCTGACACTACTGATTTGG 1110

Db 1670 TGATGTGGGTATTTTACCTATGTTGGTCCCTGTTGTTAATGCTGACACTACTGATTTGG 1729

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QY 1111 CTCTCATTTCACTCTTCAAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATC 1170
Db 1730 CTCTCATTTCACTCTTCAAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATC 1789
QY 1171 ATTATCTAGGACTTGCATTAAGATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAA 1230
Db 1790 ATTATCTAGGACTTGCATTAAGATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAA 1849
QY 1231 TCCCTGGATTTGAAGCGCAAAAGCTGAATGAAACGCCCAAAATATTTAGTAGGATTCATC 1290
Db 1850 TCCCTGGATTTGAAGCGCAAAAGCTGAATGAAACGCCCAAAATATTTAGTAGGATTCATC 1909
QY 1291 TTTAAAGGGGATTCATTTTGA- TTATACGGGGAGGGTCAAGGAAGAACCAACCTTGAC 1349
Db 1910 TTTAAAGGGGATTCATTTGATTTATACGGGGAGGGTCAAGGAAGAACCAACCTTGAC 1969
QY 1350 GTTGCAAGTGCAGTTTCAAGATCGTGTGTAGATCTTTATTTTATAGCCATGCACCTGTGTG 1409
Db 1970 GTTGCAAGTGCAGTTTCAAGATCGTGTGTAGATCTTTATTTTATAGCCATGCACCTGTGTG 2029
QY 1410 AGGAAAAATTACCTGCTTGTGACTGCGCATGTGTTCACTCACTTAAGTATTTGAAGCTGCTA 1469
Db 2030 AGGAAAAATTACCTGCTTGTGACTGCGCATGTGTTCACTCACTTAAGTATTTGAAGCTGCTA 2089
QY 1470 TGTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACCTGGTGAATA 1525
Db 2090 TGTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACCTGGTGAATA 2149
QY 1526 AAAACCTGTATATTTTACTTTGTGACAGATAGTCTGCGCCTCTGCGCAAGTGCAGA 1585
Db 2150 AAAACCTGTATATTTTACTTTGTGACAGATAGTCTGCGCCTCTGCGCAAGTGCAGA 2209
QY 1586 GATGTGTGAGCTAGAAAAA-----AAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGG 1644
Db 2210 GATGTGTGAGCTAGAAAAA-----AAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGG 2269
QY 1645 TCCGTGTAGATGTGAGATTTTCTGAAATGAAATGTTTGTGTAGACAGATCATA-CC 1703
Db 2270 TCCGTGTAGATGTGAGATTTTCTGAAATGAAATGTTTGTGTAGACAGATCATAACC 2329
QY 1704 GGTAAAGCAGGAATGACAAAGCTTCTTCTGATGCTCTGATGCTTCTAGGTGATTTGACCTTTT 1763
Db 2330 GGTAAAGCAGGAATGACAAAGCTTCTTCTGATGCTCTGATGCTTCTAGGTGATTTGACCTTTT 2389
QY 1764 ACTGTTATTAATTTGCCAATATAAGTAAATATAGATTTATATATATAGTGTGTTTCAAA 1823
Db 2390 ACTGTTATTAATTTGCCAATATAAGTAAATATAGATTTATATATATAGTGTGTTTCAAA 2449
QY 1824 AGCTTA-GACCTTTACCTTCCAGCCACCCACAGTGTGATTTTCAGAG 1873
Db 2450 AGCTTAGGACCTTTACCTTCCACCAACCACAAAGTGTGTTGATAATTCAAAG 2500
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RESULT 4

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US-09-949-016-14995
; Sequence 14995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14995
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; LENGTH: 42075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14995
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Query Match

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Best Local Similarity 44.5%; Score 996.2; DB 4; Length 42075;
Pred. No. 5e-230; Mismatches 18; Indels 4; Gaps 1;
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Matches 1021; Conservative 0;
QY 1189 ATAAGAATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAATCCCTGGATTTGAAGCGCA 1248
Db 39149 ATATTTACATTCATCTTTTCATTTTCAGATCCAAAGCAAAATCCCTGGATTTGAAGCGCA 39208
QY 1249 AAGCTGAATGAAAAAGCGCCAAATTAATTTAGTAGGATTCATCTTTTAAAGGGGATTTTCAT 1308
Db 39209 AAGCTGAATGAAAAAGCGCCAAATTAATTTAGTAGGATTCATCTTTTAAAGGGGATTTTCAT 39268
QY 1309 TTGATTATACGGGGAGGGTCAAGGAAGAACCAACCTTGACGTTGCAAGTGCAGTTTCA 1368
Db 39269 TTGATTATACGGGGAGGGTCAAGGAAGAACCAACCTTGACGTTGCAAGTGCAGTTTCA 39328
QY 1369 GATCGTTGTTAGATCTTTTATTTTATAGCCATGCACCTGTTGAGGAAATAATTTACCTGTCTT 1428
Db 39329 GATCGTTGTTAGATCTTTTATTTTATAGCCATGCACCTGTTGAGGAAATAATTTACCTGTCTT 39388
QY 1429 GACTGCCATGTGTTTCATCATCTTAAGTATTTGTAAGCTGCTATGATGATGATGATGATGAT 1488
Db 39389 GACTGCCATGTGTTTCATCATCTTAAGTATTTGTAAGCTGCTATGATGATGATGATGATGATGAT 39448
QY 1489 ATCATATCTTTTTC-----CTATCTGAGGCACCTGTTGAAATAAATAAACCCTGTATTTTAC 1544
Db 39449 ATCATATCTTTTTCCTATCTATCTGAGGCACCTGTTGAAATAAATAAACCCTGTATTTTAC 39508
QY 1545 TTTGTTGACAGATAGTCTTTCGCGCATCTTGGCAAGTTCGACAGATGCTGAGCTAGAAAA 1604
Db 39509 TTTGTTGACAGATAGTCTTTCGCGCATCTTGGCAAGTTCGACAGATGCTGAGCTAGAAAA 39568
QY 1605 AAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGTCCTGCTAGATGATGATGATGATGATGAT 1664
Db 39569 AAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGTCCTGCTAGATGATGATGATGATGATGATGAT 39628
QY 1665 TTTTCTGAAATGAAATGTTTGTGTTAGACAGATCATACCGTAAAGCAAGGATGCAAAAG 1724
Db 39629 TTTTCTGAAATGAAATGTTTGTGTTAGACAGATCATACCGTAAAGCAAGGATGCAAAAG 39688
QY 1725 CTGCTTTTCTGATGATGTTCTAGGTGATTTGTCATCTTACTGTTATATTAATTTGCCAAT 1784
Db 39689 CTGCTTTTCTGATGATGTTCTAGGTGATTTGTCATCTTACTGTTATATTAATTTGCCAAT 39748
QY 1785 ATAAGTAAATATAGATTTATATATATATATATATATATATATATATATATATATATATATAT 1844
Db 39749 ATAAGTAAATATAGATTTATATATATATATATATATATATATATATATATATATATATATAT 39808
QY 1845 GCCACCCACAGTCTGATTAATTTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1904
Db 39809 GCCACCCACAGTCTGATTAATTTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 39868
QY 1905 AGCATAAGCTAGAGGAATAATTTCTAGGAGCACTACCATCTGTTTTCACATGAA 1964
Db 39869 AGCATAAGCTAGAGGAATAATTTCTAGGAGCACTACCATCTGTTTTCACATGAA 39928
QY 1965 ATGCCACACATAGAACTCCAAACAATCAATTTTCAATTTGACAGACTGACTGTAGTTAA 2024
Db 39929 ATGCCACACATAGAACTCCAAACAATCAATTTTCAATTTGACAGACTGACTGTAGTTAA 39988
QY 2025 TTTTGTACAGAAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2084
Db 39989 TTTTGTACAGAAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 40048
QY 2085 TATCAAAATGTTTATGCAAGAAATTTATTAATTAATAAATAAATAAATAAATAAATAAATAAATAA 2144
Db 40049 TATCAAAATGTTTATGCAAGAAATTTATTAATTAATAAATAAATAAATAAATAAATAAATAAATAA 40108
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QY 1852 CACAGTGGTTGATATTTTCAGAGTCAGTCATTTGGTTATATACATGTGTAGTTCCAAAGCACAT 1911
DB 181 CACAGTGGTTGATATTTTCAGAGTCAGTCATTTGGTTATATACATGTGTAGTTCCAAAGCACAT 240
QY 1912 AAGCTAGAGAAGAATAATTTCTAGAGCAGTCATACATCTGTTTTCAAACATGAATGCCAC 1971
DB 241 AAGCTAGAGAAGAATAATTTCTAGAGCAGTCATACATCTGTTTTCAAACATGAATGCCAC 300
QY 1972 ACACATAGAACTCCAAACATCAATTTTCATTTGCACAGACTGACTGTAGTTAAATTTGTC 2031
DB 301 ACACATAGAACTCC---CAACATCAATTTTCATTTGCACAGACTGACTGTAGTTAAATTTGTC 357
QY 2032 ACAGAACTATGAGACTGAATCTAATGCTTCCAAAATGTTGTTGTTGCGAAAATATCAAA 2091
DB 358 ACAGAACTATGAGACTGAATCTAATGCTTCCAAAATGTTGTTGTTGCGAAAATATCAAA 417
QY 2092 CATTGCTATGCAAGAAATTTAATTAATACAAATGAAGATTTATACCATTTGGTTTAAAGC 2151
DB 418 CATTGCTATGCAAGAAATTTAATTAATACAAATGAAGATTTATACCATTTGGTTTAAAGC 477
QY 2152 TGTACTGAACTAAATCTGTGGAATGCATTTGTGAATGCAATTTGTGAATGCAATTTCAATAA 2208
DB 478 TGTACTGAACTAAATCTGTGGAATGCAATTTGTGAATGCAATTTGTGAATGCAATTTCAATAA 534
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RESULT 7

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US-09-513-999C-10680
; Sequence 10680, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10680
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 358
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 536
; OTHER INFORMATION: r=a or g
US-09-513-999C-10680
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Query Match 22.9%; Score 514; DB 4; Length 537;
Best Local Similarity 99.1%; Pred. No. 2e-114;
Matches 527; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1633 CACTGTGTATGTCGCGTGTAGATTCAGTCAGATTTCTGAAATGAATGTTTGTAGAC 1692
DB 1 CACTGTGTATGTCGCGTGTAGATTCAGTCAGATTTCTGAAATGAATGTTTGTAGAC 60
QY 1693 GAGATCATACCGGTAAGCAAGAAATGCAAGACTTCTTCTGCTATGTTCTAGGTGTA 1752
DB 61 GAGATCATACCGGTAAGCAAGAAATGCAAGACTTCTTCTGCTATGTTCTAGGTGTA 120
QY 1753 TTGTGACTTTTACTGTTATATTAATTTGCAATATAGTAATATATATATATATATATATAT 1812
DB 121 TTGTGACTTTTACTGTTATATTAATTTGCCAATATAGTAATATATATATATATATATAT 180
QY 1813 GTGTTTCAAAAGCTTAGACCTTTACCTTCCAGCCACCCCAAGCTGTGTATTTTCAGA 1872
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DB 181 GTGTTTCAAAAGCTTAGACCTTTACCTTCCAGCCACCCCAAGCTGTGTATTTTCAGA 240
QY 1873 GTCACTCATTTGGTTATATCATGTGTAGTTCCAAAGCACAATAAGCTAGAAAGAAATATTT 1932
DB 241 GTCACTCATTTGGTTATATCATGTGTAGTTCCAAAGCACAATAAGCTAGAAAGAAATATTT 300
QY 1933 CTAGAGCACTACCATCTGTTTTCAAACATGAATTCGCCACACATAGAACTCCAAACAACA 1992
DB 301 CTAGAGCACTACCATCTGTTTTCAAACATGAATTCGCCACACATAGAACTCC---AACA 357
QY 1993 TCAATTTTCATTTGCACAGACTGACTGTAGTTAAATTTGTCACAGATCTATGCACTGAATC 2052
DB 358 WCAATTTTCATTTGCACAGACTGACTGTAGTTAAATTTGTCACAGATCTATGCACTGAATC 417
QY 2053 TAAATGCTTCCAAAATGTTGTTTGCAAAATATCAAAACATTTGTTATGCAAGAAATTTAT 2112
DB 418 TAAATGCTTCCAAAATGTTGTTTGCAAAATATCAAAACATTTGTTATGCAAGAAATTTAT 477
QY 2113 TAAATTACAAAATGAAGATTTATACCATTTGGTTTAAAGCTGTACTGAACATAA 2164
DB 478 TAAATTACAAAATGAAGATTTATACCATTTGGTTTAAAGCTGTACTGAACATAA 529
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RESULT 8

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US-09-621-976-3840
; Sequence 3840, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3840
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..224
US-09-621-976-3840
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Query Match 21.5%; Score 482; DB 4; Length 508;
Best Local Similarity 99.4%; Pred. No. 1.1e-106;
Matches 495; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1672 AAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTGCTT 1731
DB 1 AAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTGCTT 60
QY 1732 TTCTGTTATGTTCTAGGTGTATTTGACTTTTACTGTTTATATTAATGSCCAATAAAGTA 1791
DB 61 TTCTGTTATGTTCTAGGTGTATTTGACTTTTACTGTTTATATTAATGSCCAATAAAGTA 120
QY 1792 AATATAGATTTATATATGTTATGTTTTCACAAAGCTTAGACCTTTACCTTCCAGCCACC 1851
DB 121 AATATAGATTTATATGTTATGTTTTCACAAAGCTTAGACCTTTACCTTCCAGCCACC 180
QY 1852 CACAGTGTCTCATATTTTCAGAGTCAGTCATTTGTTTATACATGTGTAGTTTCCAAAGCACAT 1911
DB 181 CACAGTGTCTCATATTTTCAGAGTCAGTCATTTGTTTATACATGTGTAGTTTCCAAAGCACAT 240
QY 1912 AAGCTAGAGAAGAATAATTTCTAGGAGCACTACCATCTGTTTTCACATGAATGCGAC 1971
DB 241 AAGCTAGAGAAGAATAATTTCTAGGAGCACTACCATCTGTTTTCACATGAATGCGAC 300
QY 1972 ACACATAGAACTCCAAACATCAATTTTCATTTGCAAGACTGACTGTAGTTAAATTTGTC 2031
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Db 934 CAGAAACCGAGAGGCCACCCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCTTTCT 993
Qy 933 GAGAGTTGGTTCAAGAGTACAGTAATTCCTCTCTTGGTCAATGGAAGTGCACGATAAAG 992
Db 994 CAGGACAGATTCAGAAAGTACACGAGCTCCCTGCGAGTTCTACGTGAACAGCACACTTAAG 1053
Qy 993 GAACCTCAGGCGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTTGG 1052
Db 1054 GAACCTGAGGAGGCTCTCTTCTGTCAGGACCTGTGTGAATTCCTTAAATTTGCAGTCTGT 1113
Qy 1053 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATTAATGCTCTGACACTACTGATTTGGCT 1112
Db 1114 ATGTGGCTCCTGACCTAGTTGGCGCTCTCTCAATGGCTGACCTGCTGCTCATGGCT 1173
Qy 1113 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAAACGCGCATCAGGCACAGATAGATCAT 1172
Db 1174 GTGGTTTCAATGTTTACTCTACCTGTAGTGTATGTTAAGCACACGAGCACAGATTTGACAA 1233
Qy 1173 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1232
Db 1234 TATCTGGGACTTGTGAGGACTTCACATAAATGCTGTGTGGCAAGATTCAGGCTAAATC 1293
Qy 1233 CCTGATTTGAAGCGCAAGCTTGAATGAA 1260
Db 1294 CCAGGCGCTAAGAGCGCCTGAGTAA 1321

RESULT 14

US-09-949-016-1127
; Sequence 1127, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1127:
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1127

Query Match 12.1%; Score 270.4; DB 4; Length 3202;
Best Local Similarity 67.3%; Pred. No. 5.7e-55;
Matches 382; Conservative 0; Mismatches 186; Indels 0; Gaps 0;
Qy 693 GTTGTGACCTCCTGTTACTGAGAGACATTAAGAAGCTGGAGTGGTGGTGGCCAGC 752
Db 1887 GCTATTGACCTGTGTATTGGCGGACATCAAGCAGCGGCATCGTTGGGAGTTTC 1946
Qy 753 CTATTCCTGCTGCTTTCATGACAGTATTCAGCATTTGACGGTAAACAGCTCATATTGCC 812
Db 1947 CTGCTGCTGCTCTTCTCCTGACCCAGTTTCAAGCGTGGTGGCGCTCGTGGCCCTACCTGSCC 2006
Qy 813 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCAGACTATC 872
Db 2007 CTGGCGGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTGTTTACAAGCAGTG 2066
Qy 873 CAGAAATCAGATGAGGCGCCACCATTCAGGGCATATCTGGAATCTGGAATGCTTATATCT 932
Db 2067 CAGAAACCGAGAGGCGCCCTTTCAAGCGCTACTTTGAGCTTTGATCATCCCTTTCT 2126
Qy 933 GAGGAGTTGGTTCAGAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACCTGCACGATAAAG 992

Db 2127 CAGAGCAGATTCAGAAAGTACACGAGCTCGCTGCGATTTCTACGTGAACAGCACACTTAAG 2186
Qy 993 GAACCTCAGGCGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTTGAAGTTTGCAGTTGG 1052
Db 2187 GAACCTGAGGAGGCTCTCTTCTGTCAGGACCTGTGTGAATTCCTTAAATTTGCAGTCTGT 2246
Qy 1053 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATTAATGCTCTGACACTACTGATTTGGCT 1112
Db 2247 ATGTGGCTCCTGACCTACCTAGTTGGCGCTCTCTTCAATGGCGCTGACCCCTGCTCATGGCT 2306
Qy 1113 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1172
Db 2307 GTGGTTTCAATGTTTACTCTACCTGTAGTGTATGTTAAGCACAGGCACAGATTTGACCA 2366
Qy 1173 TATCTAGGACTTGCATAAAGATGTTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1232
Db 2367 TATCTGGGACTTGTGAGGACTTCACATAAATGCTGTGTGGCAAGATTCAGGCTAAATC 2426
Qy 1233 CCTGATTTGAAGCGCAAGCTTGAATGAA 1260
Db 2427 CCAGGCGCTAAGAGCGCCTGAGTAA 2454

RESULT 15

US-09-439-313-279
; Sequence 279, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlock, Jennifer L.
; APPLICANT: Harlock, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 279:
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(301)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-279

Query Match 11.7%; Score 263; DB 3; Length 301;
Best Local Similarity 97.7%; Pred. No. 8.6e-54;
Matches 298; Conservative 0; Mismatches 2; Indels 5; Gaps 3;
Qy 1707 AAAGCAGGAATGACAAAGCTTGTCTTTCTGATATGTTCTAGGTGATTTGAGCTTTTACT 1766
Db 1 AAAGCAGGAATGACAAAGCTTGTCTTTCTGATATGTTCTAGGTGATTTGAGCTTTTACT 60
Qy 1767 GTTATATTAATGCGCAATATAGTAATATATATATATATATATATATATATATATATATAT 1826
Db 61 GTTATATTAATGCGCAATATAGTAATATATATATATATATATATATATATATATATATAT 120
Qy 1827 TTAGACCTTTTACCTTCCAGCCACCCACAGTGTGATTTATTTTCAAGTCACTGTTTGT 1886
Db 121 TTAGACCTTTTACCTTCCAGCCACCCACAGTGTGATTTATTTTCAAGTCACTGTTTGT 180

QY 1887 ATACATGTGTAGTTCCTCAAAGCACATAGCTAGAAAGAAATATTTCTA-GGAGCACTAC 1945
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 ATACATGTGTAGTTCCTCAAAGCACATAGCTAGAAANANANATATTTCTAGGAGCACTAC 240
QY 1946 CATCTGTTTTCACATGAAATGCCACACACATAGAACTCCACACATCAATTTCAATTGC 2005
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CATCTGTTTTC-ACATGAAATGCCACACACATAGAACTC---CAACATCAATTTCAATTGC 296
QY 2006 ACAGA 2010
Db |||||
297 ACAGA 301

Search completed: August 1, 2005, 18:14:51
Job time : 395 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-544-776-1

Perfect score: 2240

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb.in.*

4: gb.on.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2231	99.6	2235	9	AF148538 Homo sapi
2	2225	99.3	2332	9	AY102277 Homo sapi
3	2189	97.7	2276	9	AF132047 Homo sapi
4	2158	96.3	2389	9	AY102278 Homo sapi
5	1892.8	84.5	2052	9	AB015639 Homo sapi
6	1615	72.1	1728	9	BC068991 Homo sapi
7	1607.4	71.8	1610	6	BD231889 Homo sapi
8	1599	71.5	1668	9	BC026788 Homo sapi
9	1599	71.4	1619	9	AK129806 Homo sapi
10	1591.2	71.0	1654	9	BC012619 Homo sapi
11	1586.4	70.8	1694	6	CQ783030 Sequence
12	1586.4	70.8	1694	6	BD127437 Primer fo
13	1586.4	70.8	1694	9	AK075039 Homo sapi
14	1577.4	70.4	1599	6	CQ769577 Sequence
15	1574	70.3	1709	9	AB040463 Homo sapi
16	1549	69.2	1700	9	AF177332 Homo sapi
17	1548	69.1	1784	9	BC016165 Homo sapi
18	1536.4	68.6	1698	9	BC014366 Homo sapi
19	1534	68.5	1800	9	AY102276 Homo sapi

20	1533	68.4	4060	9	AY123250
21	1533	68.4	4070	9	AY123249
22	1533	68.4	4102	9	AY123245
23	1533	68.4	4109	9	AY123248
24	1533	68.4	4123	9	AY123247
25	1533	68.4	4160	9	AY123246
26	1533	68.4	4789	6	CQ874017
27	1533	68.4	4789	9	AY102279
28	1525.2	68.1	4822	6	AR220865
29	1512	67.5	1691	9	AF132048
30	1505.4	67.2	1525	9	AK130812
31	1467	65.5	1485	9	BC010737
32	1410	62.9	1617	9	AF087901
33	1409	62.9	4632	9	AF148537
34	1383.4	61.8	1466	9	BC071848
35	1319.8	58.9	2162	9	AB049853
36	1199.6	53.6	1206	9	AK172726
37	1122	50.1	1122	6	BD249448
38	1122	50.1	1122	9	HS251384
39	1097.6	49.0	2610	6	AR379837
40	1030.8	48.7	2410	10	BC070879
41	1072	47.9	2256	10	AF132046
42	1057	47.2	2782	6	AX700396
43	1057	47.2	2782	10	AY164741
44	1057	47.2	2782	10	AF132045
45	1044.4	46.6	2209	10	AY102281

ALIGNMENTS

RESULT 1
AF148538
LOCUS AF148538 2235 bp mRNA linear PRI 09-SEP-2000
DEFINITION Homo sapiens reticulon 4b mRNA, complete cds.
ACCESSION AF148538
VERSION AF148538.1 GI:10039552
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2235)
Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
AUTHORS Assignment of the human reticulon 4 gene (RTN4) to chromosome
TITLE 2p14-->2p13 by radiation hybrid mapping
JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
MEDLINE 20237542
PUBMED 10773680
REFERENCE 2 (bases 1 to 2235)
Zhou,Y., Yu,L. and Zhao,S.Y.
AUTHORS Direct Submission
TITLE Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
JOURNAL Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
P.R.China

FEATURES
source Location/Qualifiers
1..2235
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142..1263
/notes="RTN4b"
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/product="reticulon 4b"
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/db_xref="GI:10039553"
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CDS

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Db 2105 GCAAGAAATATTAAATTAACAAATGAAGATTATACCAATGTTGTTTAAAGCTGTAAGTAA 2164

Qy 2161 CTAATCTGTTGGAATGATTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2220

Db 2165 CTAATCTGTTGGAATGATTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2224

Qy 2221 TAAAAAATAA 2231

Db 2225 TAAAAAATAA 2235

RESULT 2

AY102277

LOCUS 2332 bp mRNA linear PRI 23-SEP-2003

DEFINITION Homo sapiens RTN4 isoform B1 (RTN4) mRNA, complete cds;

ACCESSION AY102277

VERSION AY102277.1 GI:26800561

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2332)

AUTHORS Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.

TITLE Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 2332)

AUTHORS Oertle, T. and Schwab, M.E.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland

REFERENCE 3 (bases 1 to 2332)

AUTHORS Van der Putten, H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland

FEATURES

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/evidence="experimental"

245..1366

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1367..2332

3'UTR

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CCACACCGCCCGGGCTCTGAGACGGCGCCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120

Db 168 CCACACCGCCCGGGCTCTGAGACGGCGCCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 227

Qy 121 ATCTCCACCCCTCCAGCCATCGAAGACCTGACACAGTCTCTCTGGTCTCTCTCTCGGACA 180

Db 228 ATCTCCACCCCTCCAGCCATCGAAGACCTGACACAGTCTCTCTGGTCTCTCTCTCGGACA 287

Qy 181 GCCACCCCGGCGGCGGCTTCAAGTACAGTTCGTTGAGGAGCCCGGAGGACGAGG 240

Db 288 GCCACCCCGGCGGCGGCTTCAAGTACAGTTCGTTGAGGAGCCCGGAGGACGAGG 347

Qy 241 AGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

Db 348 AGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 407

Qy 301 TCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360

Db 408 TCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 467

Qy 361 GCGCGCCCTGATGAGACTTCGGAATAAGTATTCGTCGCGCGCGCGCGCGCGCGCGCGCGCG 420

Db 468 GCGCGCCCTGATGAGACTTCGGAATAAGTATTCGTCGCGCGCGCGCGCGCGCGCGCGCGCG 527

Qy 421 CGCGCGCTCCCGCTCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480

Db 528 CGCGCGCTCCCGCTCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 587

Qy 481 CGACCGTGCCTCGCGCGCATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Db 588 CGACCGTGCCTCGCGCGCATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647

Qy 541 AGACGAGAGCTTCGCGCGCGCGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600

Db 648 AGACGAGAGCTTCGCGCGCGCGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 707

Qy 601 CAGACCCGCTGTGAGACCCCG 660

Db 708 CAGACCCGCTGTGAGACCCCG 767

Qy 661 CGCCCAAGCGCAGCGGCTCTCTCGGGCTCAGTGGTGTGTGACCTCTCTCTCTCTCTCTCTCTCT 720

Db 768 CGCCCAAGCGCAGCGGCTCTCTCGGGCTCAGTGGTGTGTGACCTCTCTCTCTCTCTCTCTCTCT 827

Qy 721 TTAAGAAGACTGAGTGGT 780

Db 828 TTAAGAAGACTGAGTGGT 887

Qy 781 TCAGCATTTGAGCGGTAAAGCCCTACATTCCTCTTGGCCCTGCTCTCTCTCTCTCTCTCTCTCT 840

Db 888 TCAGCATTTGAGCGGTAAAGCCCTACATTCCTCTTGGCCCTGCTCTCTCTCTCTCTCTCTCTCT 947

Qy 841 TTAGGATATACAAAGGCTGATCCAGCTATCCAGAAATCAGATGAAGGAGGAGGAGGAGGAGGAG 900

Db 948 TTAGGATATACAAAGGCTGATCCAGCTATCCAGAAATCAGATGAAGGAGGAGGAGGAGGAGGAG 1007

Qy 901 GGGCATATCTGGAATCTGAAGTGTCTATATCTGAGGAGTGGTGTGTGTGTGTGTGTGTGTGTGT 960

Db 1008 GGGCATATCTGGAATCTGAAGTGTCTATATCTGAGGAGTGGTGTGTGTGTGTGTGTGTGTGTGT 1067

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1128	Db	ATTTTAGTTGATTTCTCTGAAGTTTGCAGTGTGGATGTGGGTATTTTACCTATGTTGGTGCCT	1187
1081	Qy	TGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTTCACTTTCAGTGTTCCTGTGTTA	1140
1188	Db	TGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTTCACTTTCAGTGTTCCTGTGTTA	1247
1141	Qy	TTTATGAACGGCATCAGCGACAGATAGATCATTTATCTAGAGCTTGCAGATTAAGATGTGTTA	1200
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1201	Qy	AAGATGCTATGGCTTAAATCAAGCAAAAAATCCCTCGATTTGAAGCGCAAAAGCTGAATGAA	1260
1308	Db	AAGATGCTATGGCTTAAATCAAGCAAAAAATCCCTCGATTTGAAGCGCAAAAGCTGAATGAA	1367
1261	Qy	AACGCCCAAAATAATTAGTAGGAGTTTCACTTTTAAAGGGGATATTCATTTGATTTATACGG	1320
1368	Db	AACGCCCAAAATAATTAGTAGGAGTTTCACTTTTAAAGGGGATATTCATTTGATTTATACGG	1427
1321	Qy	GGGAGGCTCAGGGAAGCAACGACCTTGACGTTGCGAGTTCAGAGTTCACAGATCGTTGTAG	1380
1428	Db	GGGAGGCTCAGGGAAGCAACGACCTTGACGTTGCGAGTTCAGAGTTCACAGATCGTTGTAG	1487
1381	Qy	ATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTAACCTGTCTTGACTGCGCATGTG	1440
1488	Db	ATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTAACCTGTCTTGACTGCGCATGTG	1547
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1548	Db	TTTCATCATCTTTAAGTATTTGTAAGCTGCTATGTATGGATTTTAAACCGTAAATCATATCTTTT	1607
1501	Qy	TCCTTATCTGAGGCACTGGTGGATAAAAAACCTGTATATTTTACTTTGTTGCGAGATGTC	1560
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1561	Qy	TTGCGCGATCTTTGGCAAGTTTGACAGATGTGGAGCTTAGAAAAAATAAAAAAAGCCCT	1620
1668	Db	TTGCGCGATCTTTGGCAAGTTTGACAGATGTGGAGCTTAGAAAAAATAAAAAAAGCCCT	1727
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1728	Db	TTTCAGTTTGTGCACTGTATGGTCCGTGTAGATTCGATCGAGATTTTCTGAAATGAAAT	1787
1681	Qy	GTTTGTTTAGCGAGATCATACCGGTAAAGCAGGAATGCAAAAGCTTGCTTTCTGTGTAT	1740
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1848	Db	GTTCCTAGGTGATTTGCACTTTTACTGTATATTTAAATTTGCCAATATAAGTAAATATAGAT	1907
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1908	Db	TATATATGTATAGTTGTTTCAAAAAGCTTAGACCTTTTACCTTTCCAGGCCACCCACAGTGCT	1967
1861	Qy	TGATATTTTCAGAGTCAGTGCATTTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAA	1920
1968	Db	TGATATTTTCAGAGTCAGTGCATTTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAA	2027
1921	Qy	GAAGAAATATTTCTAGGAGCACTACCATCTGTTTTTCAACATGAAATGCCACACACATAGA	1980
2028	Db	GAAGAAATATTTCTAGGAGCACTACCATCTGTTTTTCAACATGAAATGCCACACACATAGA	2087
1981	Qy	ACTCCAAACACATCAAATTTCAATTCACAGACTGACTGTAGTTAATTTTGTCCAGAAATCT	2040
2088	Db	ACTCCAAACACATCAAATTTCAATTCACAGACTGACTGTAGTTAATTTTGTCCAGAAATCT	2147
2041	Qy	ATGAGCTGAATCTAATGCTTCCAAAAATGTTTGTGTTGTTGCAAAATATCAAAATTTGTTAT	2100
2148	Db	ATGAGCTGAATCTAATGCTTCCAAAAATGTTTGTGTTGTTGCAAAATATCAAAATTTGTTAT	2207

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Qy      2101 GCAAGAAATTTAATTACAAAATGAAGATTATATACCATTTGGTGTGCTTAAGCTGTACTGAA   2160
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Qy      2161 CTAATCTGTGGNATGCATTTGTGAATCTGTATTAAGAAGCAAGTATCAATAAAGCTTATAGACT   2220
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Db      2268 CTAATCTGTGSAATGCATTTGTGAATCTGTATTAAGAAGCAAGTATCAATAAAGCTTATAGACT   2327

Qy      2221 TAAAA 2225
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Db      2328 TAAAA 2332

RESULT 3
AF132047          2276 bp    mRNA       linear     PRI 18-MAY-1999
LOCUS             Homo sapiens foocen-m mRNA, complete cds.
DEFINITION        AF132047
ACCESSION         AF132047
VERSION           AF132047.1 GI:4838516
KEYWORDS
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1 (bases 1 to 2276)
AUTHORS           Ito,T. and Schwartz,S.M.
TITLE             Cloning of a member of the reticulon gene family in human:
                  ubiquitous type
JOURNAL            Unpublished
REFERENCE         2 (bases 1 to 2276)
AUTHORS           Ito,T. and Schwartz,S.M.
TITLE             Direct Submission
JOURNAL            Submitted (27-FEB-1999) Pathology, University of Washington, 1959
                  Pacific NE, Seattle, WA 98195, USA
FEATURES           Location/Qualifiers
source            1..2276
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ORIGIN
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Best Local Similarity    99.5%; Pred.No. 0;
Matches 2230; Conservative 0; Mismatches 0; Indels 11; Gaps 3;

Qy      1 CGTCACCACAGTAGTGCCCTCGGCTCAGTCGGGCCCGAGCCCCCTCTCAGTCTCCCCAACCC   60
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Qy      61 CCACAACCGCCCGGGGCTCTGAGACGGGCCCGGGCGGGCGGCGGAGCAGTCGAGCATC   120
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Qy      121 ATCTCCACCTTCAGCCATCGAAGACCTGACACAGTCTCCTCTGGTCTCGTCTCGGACA   180
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Qy      181 GCCCACCCCGCGCGACCGCGCTTCAAGTACAGTTCTGTGAGGGAGCCCGAGACGAGG   240

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[illegible]

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Db	1363	GG	GAGGGTCAGGGAAGAAC	GAACCTTGACGTTGCGAGTGCAGTTTTCACAGATCGTTGTTAG	1422
Qy	1381	AT	CTTTATTTTTAGCCAT	GCACCTGTTGTGAGGAAAAATTACCTGTCTTGATGCCATGTG	1440
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Qy	1441	TT	CATCATCTTTAGTAT	TGTTAAAGCTGCTATGTATGGATTTTAAACCGTAATCATATCTTTT	1500
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Db	1603	AG	CTTCCCGCATCTTGG	CAAGTTGTCAGAGATGGTGGAGCTAGAAAAAAAATAAAG	1658
Qy	1617	CC	CTTTTTCAGTTTGTG	CACCTGTGTATGGTCCGCTGATGTTGATGCAGATTTTCTGGAATG	1676
Db	1659	CC	CTTTTTCAGTTTGTG	CACCTGTGTATGGTCCGCTGATGTTGATGCAGATTTTCTGGAATG	1718
Qy	1677	AA	TGTTTGTTTAGAC	CGAGATCATACCGGTAAAGCAGAGAAATGACAAAGCTTGCTTTTCTG	1736
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Qy	1737	GT	ATGTTCTTAGGTGTA	TGTGACTTTTACTGTTTATATTAATTTGCGCAATATAAGTAAATAT	1796
Db	1779	GT	ATGTTCTTAGGTGTA	TGTGACTTTTACTGTTTATATTAATTTGCGCAATATAAGTAAATAT	1838
Qy	1797	AG	ATTATATATGATAG	TGTTTTCACAAAGCTTAGACCTTTTACCTTCCAGCCACCCACAG	1856
Db	1839	AG	ATTATATATGATAG	TGTTTTCACAAAGCTTAGACCTTTTACCTTCCAGCCACCCACAG	1898
Qy	1857	TG	CTTGATATTTTCAG	AGTCAAGTCAATTTGTTTATACATGTTAGTTTCCAAAGCACATAGCT	1916
Db	1899	TG	CTTGATATTTTCAG	AGTCAAGTCAATTTGTTTATACATGTTAGTTTCCAAAGCACATAGCT	1958
Qy	1917	AG	AAGAAGAAATATTT	CTAGGAGCATACATCTGTTTTCACATGGAATGCCACACACA	1976
Db	1959	AG	AAGAAGAAATATTT	CTAGGAGCATACATCTGTTTTCACATGGAATGCCACACACA	2018
Qy	1977	TAG	AACTCCCAACAACAT	CAATTTTCATTTGACAGACTGACGTAGTTAAATTTTGTTCACAGA	2036
Db	2019	TAG	AACTC---CAACAT	CAATTTTCATTTGACAGACTGACGTAGTTAAATTTTGTTCACAGA	2075
Qy	2037	AT	CTATGGA	CTGAATCTAAATGCTTCCAAAAATGTGTTGTTTTCGCAAAATATCAAAATG	2096
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Qy	2097	TT	ATGCAAGAAATTTAT	TATTAATTCAAAATGAAGATTTTATACCATGTGGTTTAAGCTGTAC	2156
Db	2136	TT	ATGCAAGAAATTTAT	TATTAATTCAAAATGAAGATTTTATACCATGTGGTTTAAGCTGTAC	2195
Qy	2157	TGA	CTAAATCTGTGGA	ATCATTTGTGAACTGTAAAGCAAAAGTATCAATAAAGCTTTATA	2216
Db	2196	TGA	CTAAATCTGTGGA	ATCATTTGTGAACTGTAAAGCAAAAGTATCAATAAAGCTTTATA	2255
Qy	2217	GAC	TTAAAAAATAAAAAA	AAAAA 2237	
Db	2256	GAC	TTAAAAAATAAAAAA	AAAAA 2276	

RESULT 4	
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LOCUS	AV102278 2389 bp mRNA linear PRI 23-SEP-2003
DEFINITION	Homo sapiens RTN4 isoform B2 (RTN4) mRNA, complete cds; alternatively spliced.
ACCESSION	AV102278

AV102278.1	GI:26800568
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	
AUTHORS	1 (bases 1 to 2389)
TITLE	Oertle,T., Huber,C., van der Putten,H. and Schwab,M.B.
	Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4
JOURNAL	J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE	22376540
PUBMED	12488097
REFERENCE	2 (bases 1 to 2389)
AUTHORS	Oertle,T. and Schwab,M.E.
TITLE	Direct Submission
JOURNAL	Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland
REFERENCE	3 (bases 1 to 2389)
AUTHORS	Van der Putten,H.
TITLE	Direct Submission
JOURNAL	Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
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3'UTR	1424..2389
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Best Local Similarity	97.5%; Pred. No. 0;
Matches 2225; Conservative	0; Mismatches 0; Indels 57; Gaps 1;
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Db	108 CGTCACACAGTAGGTCCCTCGGCTCAGTCGGCCAGCCCTCTCAGTCCTCCCCAACCC 167
Qy	61 CCACAACGCCCGCGGCTCTGAGACGCGGCCCGCGCGCGGCGGAGCAGCTGCAGCATC 120
Db	168 CCACAACGCCCGCGGCTCTGAGACGCGGCCCGCGCGCGGCGGAGCAGCTGCAGCATC 227
Qy	121 ATCTCCACCTCCAGCCATGAAGACCTGGACCACTCTCCTCGTCTCGTCTCGGACA 180
Db	228 ATCTCCACCTCCAGCCATGAAGACCTGGACCACTCTCCTCGTCTCGTCTCGGACA 287
Qy	181 GCCCACCCCGCGCAGCCGCGCTTCAAGTACCAGTTCTGTGAGGAGCGCCGAGGACGAGG 240

Db	288	 GCCACCCCGCGCAGCCCGGTTCAAGTACCAGTTCTGTGAGGAGCCCGAGGACGAGG	347
QY	241	AGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGAAGCCTTGAGGAGAGCTGGAAGTGC	300
Db	348	AGGAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGAAGCCTTGAGGAGAGCTGGAAGTGC	407
QY	301	TGGAGAGGAAGCCGCGCGCGGCTGTGTCGGCGGCCCAAGTGCACACGCGCCCTGCGCGCG	360
Db	408	TGGAGAGGAAGCCGCGCGCGGCTGTGTCGGCGGCCCAAGTGCACACGCGCCCTGCGCGCG	467
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RESULT 6
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LOCUS
DEFINITION Homo sapiens reticulon 4, transcript variant 2, mRNA (cdna clone
IMAGE:4634289), complete cds.
ACCESSION BC068991
VERSION BC068991.1 GI:46362518
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1728)
AUTHORS
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Udwin,T.B., Toshitoki,S.,
Carinci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
```

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1728)

Strausberg, R.

Direct Submission

Submitted (05-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prähbu, Parvaneh Saeedi, JR Santos, Angelique Schmerch, Ursula Skalska, Duane Smallos, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 54 Row: c Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28557782
This clone has the following problem: The cds is short compared to the longest cds in the locus.

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RESULT 7
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LOCUS BD231889
DEFINITION Bone marrow secreted proteins and polynucleotides.
ACCESSION BD231889
VERSION BD231889.1 GI:33041659
KEYWORDS JP 2002511231-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Lin,H. and Cao,L.
TITLE Bone marrow secreted proteins and polynucleotides
JOURNAL Patent: JP 2002511231-A 3 16-APR-2002;
CHIRON CORP
OS Homo sapiens (human)
PN JP 2002511231-A/3
PD 16-APR-2002
PF 18-DEC-1998 JP 2000526635
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Query Match 71.8%; Score 1607.4; DB 6; Length 1610;
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Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ACCESSION AKI29806.1 GI:34526422
VERSION
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS
Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Suzuki, Y.,
Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M.,
Sugiyama, T., Irie, R., Otsuki, F., Sato, H., Nishikawa, T.,
Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
1 Unpublished
2 (bases 1 to 1619)
Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: fildna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB, clone selection for
full insert sequencing: RAB and Helix Research Institute.
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SOURCE     Homo sapiens
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AUTHORS   Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Aramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
```


Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1654)
 Direct Submission
 Strausberg, R.
 Submitted (15-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadnan@systemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 19 Row: d Column: 8
 This clone was selected for full length sequencing because it
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VERSION CQ783030.1 GI:45502969
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ORGANISM Homo sapiens
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Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
Koga, H.
TITLE Primers for synthesizing full length cDNA clones and their use
JOURNAL Patent: EP 1396543-A 3170 10-MAR-2004;
Research Association for Biotechnology (JP)
FEATURES
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Best Local Similarity 99.9%; Pred. No. 3.1e-265;

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VERSION BD127437.1 GI:23222382
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Primer for synthesizing full-length cDNA and use thereof
Patient: JP 2002017375-A 2868 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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PD 22-JAN-2002
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SHINICHI KOJIMA,
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AUTHORS Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Sato, H., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahara, K., Masuko, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1694)
AUTHORS Isogai, T. and Otsuki, T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(2-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of

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Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).

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Query Match 70.8%; Score 1586.4; DB 9; Length 1694;
 Best Local Similarity 99.9%; Pred. No. 3.1e-265;
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AUTHORS	Koenig-Hoffman, K., Kazinski, M., Schaefer, R., and Kesner, B.		

TITLE JOURNAL	Novel apoptosis-inducing dna sequences									
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DEFINITION Homo sapiens mRNA for RTN-XS, complete cds.
ACCESSION AB040463
VERSION AB040463.1 GI:11610576
KEYWORDS reticulon.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.
A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
endoplasmic reticulum and reduces their anti-apoptotic activity
Oncogene 19 (50), 5736-5746 (2000)
21010696
MEDLINE
PUBMED 11126360
REFERENCE 2 (bases 1 to 1709)
AUTHORS Eguchi,Y., Tagami,S. and Tsujimoto,Y.
DIRECT SUBMISSION
TITLE Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate
JOURNAL School of Medicine, Biomedical Research Center, Department of

Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan
(E-mail:eguchi@gen.med.osaka-u.ac.jp, Tel: +81-6-6879-3363,
Fax: +81-6-6879-3369)
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ORIGIN
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Best Local Similarity 99.4%; Pred. No. 4.4e-263;
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Qy 181 GCCACACCGCCCGGCGGCTTCAAGTTCACAGTTCGTCGAGGAGCCCGAGGACGAGG 240
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Db		828	TTAAGAAGACTGGAGTGGTGGTGGTGGCCAGCCTATTCCTGTGCTCTTCATTGACAGTAT	887
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2005, 10:33:13 ; Search time 1113 Seconds
(without alignments)
11913.945 Million cell updates/sec

Title: US-09-544-776-1
Perfect score: 2240
Sequence: 1 cgtcacacagtggttcct.....taaaaaaaaaaaaaaaaaa 2240

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: Geneseqn2001bs.*
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9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1607.4	71.8	1610	3 AAZ36230	AAZ36230 cDNA enco
5	1586.4	70.8	1694	4 AAK94408	AAK94408 Human ful
6	1586.4	70.8	1694	12 ADL31137	ADL31137 Full leng
7	1581	70.6	1758	4 AAF32725	AAF32725 Human sec
8	1577.4	70.4	1599	10 ADI62860	ADI62860 Human apo
9	1533	68.4	4789	13 ADR83534	ADR83534 Human ret
10	1525.2	68.1	4822	6 ABS70449	ABS70449 Human bon
11	1488.8	66.5	1798	6 ABK90135	ABK90135 DNA encod
12	1473.4	65.8	1514	6 ABK34580	ABK34580 Human cdn
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14	1409	62.9	4632	6 ABV94680	ABV94680 Human pan
15	1409	62.9	4632	10 ADG32772	ADG32772 Human DNA
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17	1325	59.2	4698	8 ABX34563	ABX34563 Human mdd
18	1216	54.3	1216	6 ABA05903	ABA05903 Human RTN
19	1122	50.1	1122	3 AAZ56888	AAZ56888 Human MAG
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27	923	41.2	4093	2 AAZ23454	AAZ23454 cDNA enco
28	907	40.5	3919	12 ADF45550	ADF45550 Human Nog
29	907	40.5	4053	4 AAS09453	AAS09453 Human CDN
30	907	40.5	4053	9 ACC81048	ACC81048 Human CG
31	907	40.5	4053	12 ADP13574	ADP13574 Renal cel
32	906.8	40.5	994	12 ADP18854	ADP18854 Human sec
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38	800	35.7	3535	4 AAH72837	AAH72837 Human cer
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ALIGNMENTS

RESULT 1
AAC64406
ID AAC64406 standard; cDNA; 2240 BP.
XX AAC64406;
AC AAC64406;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human Nogo B nucleotide sequence SEQ ID NO:1.
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KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
KW stress-phosphorylated endoplasmic reticulum protein; cytosolic;
KW gene therapy; cell growth; cellular stress response; neuron growth;
KW regulator of oxidative stress; inhibitor of neurite outgrowth;
KW axon regeneration; diagnosis; cancer; identification; ss.
OS Homo sapiens.
XX
PN WO200060083-A1.
XX
PD 12-OCT-2000.
XX
PF 07-APR-2000; 2000WO-US009383.
XX
PR 08-APR-1999; 99US-0128372P.
PR 21-JUN-1999; 99US-0140331P.
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PA (CHIR) CHIRON CORP.
XX
PI Wei D, Halenbeck R, Williams LT;
XX
DR WPI; 2000-665007/64.
DR P-PSDB; AAB24242.
XX
PT Novel protein associated with cell stress response useful for modulating
PT stress levels, cell growth, diagnosis and treatment of cancer and
PT malignant growth and for identifying agonists and antagonists.
XX
PS Claim 2; Page 63-64; 68pp; English.
XX
CC The present sequence encodes a human stress-phosphorylated endoplasmic
CC reticulum protein, designated Nogo B. Nogo B has cytosolic activity and
CC is a modulator of the storage and exchange of calcium, cell growth and

cellular stress response. It can: regulate oxidative stress; inhibit neurite outgrowth, neuron growth and axon regeneration. Nogo B polypeptides and polynucleotides are useful for modulating stress levels and cellular stress-response, cell growth and viability, diagnosis and treatment of cancer, malignant growth and other Nogo B related diseases. Nogo B polypeptides are also useful to screen combinatorial libraries to identify agonist or antagonist. Antibodies against Nogo B polypeptides are useful for affinity chromatography and distinguishing Nogo B polypeptides

Query Match 99.9%; Score 2238.4; DB 3; Length 2240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1021 ATTTAGTTGATCTCTGAAGTTTCAGTGTGATGTTGGTATTTACCTATGTTGGTGCT 1080

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DB 1081 TGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTA 1140

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DB 1201 AAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGA 1260

QY 1261 AACCCCAAAATATAGTAGGATTCATCTTTAAAGGGGATTCATTTGATATATACGG 1320

DB 1261 AACCCCAAAATATAGTAGGATTCATCTTTAAAGGGGATTCATTTGATATATACGG 1320

QY 1321 GGGAGGGTTCAGGGAAGAACGAACTTGAAGTTCAGTGCAGTTCACAGATCGTTGTTAG 1380

DB 1321 GGGAGGGTTCAGGGAAGAACGAACTTGAAGTTCAGTGCAGTTCACAGATCGTTGTTAG 1380

QY 1381 ATCTTTATTTTACGCATGCACTGTTGTGAGGAAATTAATCTGCTTCAGTGCATGTC 1440

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DB 1621 TTTTCAGTTTGTGCACTGTTGATGTTGCTGTAGATTGATGAGATTTTCTGAAATGAAT 1680

QY 1681 GTTTGTTTGTAGACGAGATCATACCGGTAAAGCAGGAAATGACAAAGCTTCTCTTCTG 1740

DB 1681 GTTTGTTTGTAGACGAGATCATACCGGTAAAGCAGGAAATGACAAAGCTTCTCTTCTG 1740

QY 1741 GTTCTAGGTGTTTGTGACTTTTACTGTTATATTAATTTGCCAATATTAAGTAATATAGAT 1800

DB 1741 GTTCTAGGTGTTTGTGACTTTTACTGTTATATTAATTTGCCAATATTAAGTAATATAGAT 1800

QY 1801 TATATATGATAGTGTGTTTTCACAAAGCTTTCAGTCTTTTACCTTCCAGCCACCCACAGT 1860

DB 1801 TATATATGATAGTGTGTTTTCACAAAGCTTTCAGTCTTTTACCTTCCAGCCACCCACAGT 1860

QY 1861 TGATATTTTTCAGAGTCAGTTCATTGGTGTATATGATGTAGTTCCTTCCAAAGCAATAGCT 1920

DB 1861 TGATATTTTTCAGAGTCAGTTCATTGGTGTATATGATGTAGTTCCTTCCAAAGCAATAGCT 1920

QY 1921 GAAGAAATATTTTTCAGGAGCTACCATCTGTTTCAACATGAAATGCGCACACATAGA 1980

1921	GAAGAAATATTTCTAGAGCAGTACCATCTGTTTTCAACATGAATGCCACACATAGA	1980
1981	ACTCCAAACAATCAATTTTCATTCGACAGACTGACTGTAGTAAATTTTGTGCAGAAATCT	2040
1981	ACTCCAAACAATCAATTTTCATTCGACAGACTGACTGTAGTAAATTTTGTGCAGAAATCT	2040
2041	ATGGACTGAATCTAAATGCTTTCCAAAAATGTTTGTTCGCAAAATATCAAAACATTTGTTAT	2100
2041	ATGGACTGAATCTAAATGCTTTCCAAAAATGTTTGTTCGCAAAATATCAAAACATTTGTTAT	2100
2101	GCAAGAAATTTAAATPACAAAATGAAGATTTATACCATTTGTGGTTTAAAGCTGTACTGAA	2160
2101	GCAAGAAATTTAAATPACAAAATGAAGATTTATACCATTTGTGGTTTAAAGCTGTACTGAA	2160
2161	CTAAATCTGTGGGAATGCATTTGCAATGTGTAATGAAGCAAGATATCAATAAAGCTTTATAGACT	2220
2161	CTAAATCTGTGGGAATGCATTTGCAATGTGTAATGAAGCAAGATATCAATAAAGCTTTATAGACT	2220
2221	TAATAAAAAAAAAAAAAAAAAAAAAA	2240
2221	TAATAAAAAAAAAAAAAAAAAAAAAA	2240

RESULT 2	
ABV94681	
ID	ABV94681 standard; cDNA; 2235 BP.
XX	
XX	ABV94681;
AC	
XX	
DT	14-JAN-2003 (first entry)
XX	
XX	Human pancreatic cancer expressed cDNA SEQ ID NO 54.
DE	
XX	
KW	Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW	cytostatic; tumour; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200260317-A2.
XX	
PD	
XX	08-AUG-2002.
XX	
XX	30-JAN-2002; 2002WO-US002781.
XX	
XX	30-JAN-2001; 2001US-0265305P.
PR	31-JAN-2001; 2001US-0265682P.
PR	09-FEB-2001; 2001US-0267568P.
PR	21-MAR-2001; 2001US-0278651P.
PR	28-APR-2001; 2001US-0287112P.
PR	16-MAY-2001; 2001US-0291631P.
PR	12-JUL-2001; 2001US-0305484P.
PR	20-AUG-2001; 2001US-0313999P.
PR	27-NOV-2001; 2001US-0333626P.
PR	

PA (CORI-) CORIYA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI
XX
XX WPI: 2002-627435/67.
DR P-PSDB; ABP68601.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.

The invention relates to an isolated polynucleotide (I) comprising: (a)
 any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 complements of (a); (c) sequences consisting of at least 20 contiguous
 residues of (a); (d) sequences that hybridize to (a), under moderately
 stringent conditions; (e) sequences having at least 75% or 90% identity
 to (a); or (f) degenerate variants of (a). Polypeptides (ASP68596-
 ASP69599)

CC	ABP68637)	encoded by (I) and oligonucleotide can be used to detect cancer
CC	in a patient and compositions comprising polypeptides, polynucleotides,	
CC	antibodies, fusion proteins, T cell populations and antigen presenting	
CC	cells expressing the polypeptide are useful in treating pancreatic cancer	
CC	and stimulating an immune response. The polynucleotides can be used as	
CC	probes or primers for nucleic acid hybridisation, in the design and	
CC	preparation of ribozyme molecules for inhibiting expression of the tumour	
CC	polypeptides and proteins in the tumour cells, in vaccines and for gene	
CC	therapy. Note: The sequence data for this patent did not form part of the	
CC	printed specification, but was obtained in electronic format directly	
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 2235 BP; 562 A; 560 C; 537 G; 576 T; 0 U; 0 Other;	
	Query Match	99.6%; Score 2231; DB 6; Length 2235;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 2231; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	CGTCAACACAGTAGTTCCTTCGGCTCAGTCGGCCGACGCCCTCTCAGTCTCTCCCAACCC 60
Db	5	CGTCACCACACAGTAGTTCCTTCGGCTCAGTCGGCCGACGCCCTCTCAGTCTCTCCCAACCC 64
Qy	61	CCACACCGCCCGCGGCTCTGAGACGCGGCCCGCGGGCGCGGACGACGTGACGATC 120
Db	65	CCACACCGCCCGCGGCTCTGAGACGCGGCCCGCGGGCGCGGACGACGTGACGATC 124
Qy	121	ATCTCCACCCTCCAGACCATCGAAGACCTGACACAGTCTCCTCTGGTCTCTGCTCTCGGACA 180
Db	125	ATCTCCACCCTCCAGCCATGGAAGACTTGACACAGTCTCCTCTGGTCTCTGCTCTCGGACA 184
Qy	181	GCCACACCCCGCGCGACGCCGCTTCAAGTACACAGTTCTGTGAGGAGGCCCGAGGACGAGG 240
Db	185	GCCACACCCCGCGCGACGCCGCTTCAAGTACACAGTTCTGTGAGGAGGCCCGAGGACGAGG 244
Qy	241	AGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db	245	AGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 304
Qy	301	TGAGAGGAAGACCCGCGCGCGGCTGTCTCCGCGGCCCGAGTGTCCACACGCGCCCTGCGCCG 360
Db	305	TGAGAGGAGAGCCGCGCGCGGCTGTCTCCGCGGCCCGAGTGTCCACACGCGCCCTGCGCCG 364
Qy	361	GCGCGCCCTTGATGGAATTTCGGAATAATGACTTGTGTGCGCGCGCGGCCCGGGAGACCCCTGC 420
Db	365	GCGCGCCCTTGATGGAATTTCGGAATAATGACTTGTGTGCGCGCGCGGCCCGGGAGACCCCTGC 424
Qy	421	CGGCGGCTCCCCCGTCCCGCGGAGCGGCGAGCGGTCTTGGGACCGGAGCGCGGTGTCTGT 480
Db	425	CGGCGGCTCCCCCGTCCCGCGGAGCGGCGAGCGGTCTTGGGACCGGAGCGCGGTGTCTGT 484
Qy	481	CGACCGTGC CGCGCCATATCCCGCTGTCTGTCTGCGGAGTCTGCGCCCTCAAAGTCTCCCTG 540
Db	485	CGACCGTGC CGCGCCATATCCCGCTGTCTGTCTGCGGAGTCTGTGCGCCCTCAAAGTCTCCCTG 544
Qy	541	AGGACGACGAGCTTCGCGCCCGGCTCCCTCTCTCCCGCGGAGCGGTGAGCCCCCAGG 600
Db	545	AGGACGACGAGCTTCGCGCCCGGCTCCCTCTCTCCCGCGGAGCGGTGAGCCCCCAGG 604
Qy	601	CAGAGCCCGTGTGACACCCCGCGAGCCCGGCTCTCCGCGCGCGCCCTCTCACCCCGCGCG 660
Db	605	CAGAGCCCGTGTGACACCCCGCGAGCCCGGCTCTCCGCGCGCGCCCTCTCACCCCGCGCG 664
Qy	661	CGCCCAAGCGCAGGGGCTCTCGGGCTCAGTGGTTGTGACCTCTCTACTGGAGAGACA 720
Db	665	CGCCCAAGCGCAGGGGCTCTCTCGGGCTCAGTGGTTGTGACCTCTCTACTGGAGAGACA 724
Qy	721	TTAAGAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGTCTGCTTTCATTCAGCAT 780
Db	725	TTAAGAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGTCTGCTTTCATTCAGCAT 784
Qy	781	TCAGCATTTGTGAGGTAAACGCTACATTCGCTTTGGCCCTGCTCTGTGTACCATTCAGCT 840
Db	785	TCAGCATTTGTGAGGTAAACGCTACATTCGCTTTGGCCCTGCTCTGTGTACCATTCAGCT 844

QY 841 TTAGGATATACAAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCA 900
Db 845 TTAGGATATACAAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCA 904
QY 901 GGGCATATCTGGAATCTCAAGTGTGTATATCTGAGGAGTGTGGTTCAGAAAGTACAGTAAT 960
Db 905 GGGCATATCTGGAATCTCAAGTGTGTATATCTGAGGAGTGTGGTTCAGAAAGTACAGTAAT 964
QY 961 CTGCTCTTGGTCACTGTAAGTGCAGATAAAGGAATCAGAGCGCTCTCTTCTAGTTGATG 1020
Db 965 CTGCTCTTGGTCACTGTAAGTGCAGATAAAGGAATCAGAGCGCTCTCTTCTAGTTGATG 1024
QY 1021 ATTTAGTTGATCTCTGAAATTTGCAGTGTGATGTGGGTATTTACCTATGTGTGGTCT 1080
Db 1025 ATTTAGTTGATCTCTGAAATTTGCAGTGTGATGTGGGTATTTACCTATGTGTGGTCT 1084
QY 1081 TGTTAATGGTCTGACACTGATCTTTGGCTCTCAATTTCACTCTTCACTGTCTCTGTTA 1140
Db 1085 TGTTAATGGTCTGACACTGATCTTTGGCTCTCAATTTCACTCTTCACTGTCTCTGTTA 1144
QY 1141 TTTATGAACGGCATCAGGCACAGATAGATCAATATCTAGGACTTGCAAAATGAAGATGTTA 1200
Db 1145 TTTATGAACGGCATCAGGCACAGATAGATCAATATCTAGGACTTGCAAAATGAAGATGTTA 1204
QY 1201 AAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGAA 1260
Db 1205 AAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGAA 1264
QY 1261 AACGCCAAAATAATTAGTAGAGTTCATCTTTAAAGGGGATATTCATTTGATATACGG 1320
Db 1265 AACGCCAAAATAATTAGTAGAGTTCATCTTTAAAGGGGATATTCATTTGATATACGG 1324
QY 1321 GGGAGGGTCAGGAAGAAGCAACCTTGACGTTGACGTCAGTTCACAGATCGTTGTTAG 1380
Db 1325 GGGAGGGTCAGGAAGAAGCAACCTTGACGTTGACGTCAGTTCACAGATCGTTGTTAG 1384
QY 1381 ATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTAACCTGCTTTGACTGCCATGTG 1440
Db 1385 ATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTAACCTGCTTTGACTGCCATGTG 1444
QY 1441 TTCATCATCTTAAAGTATTTGTAAGCTGCTATGTATGGATTTAAACCGTAAATCATATCTTTT 1500
Db 1445 TTCATCATCTTAAAGTATTTGTAAGCTGCTATGTATGGATTTAAACCGTAAATCATATCTTTT 1504
QY 1501 TCCTATCTGAGCACTGCTGGAATAAAAAACCTGATATATTTTACTTTCTGTCAGATAGTC 1560
Db 1505 TCCTATCTGAGCACTGCTGGAATAAAAAACCTGATATATTTTACTTTTGTGAGATAGTC 1564
QY 1561 TTGCGCATCTTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAATAAAAAAGCCCT 1620
Db 1565 TTGCGCATCTTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAATAAAAAAGCCCT 1624
QY 1621 TTTCAAGTTGTGCACTGTATGTCCTGTAGATTTGATGAGATTTTCTGAAATGAAT 1680
Db 1625 TTTCAAGTTGTGCACTGTATGTCCTGTAGATTTGATGAGATTTTCTGAAATGAAT 1684
QY 1681 GTTTGTTTGTAGACGATCATACCGGTAAGCAGGAATGACAAAGCTGCTTTCTGCTAT 1740
Db 1685 GTTTGTTTGTAGACGATCATACCGGTAAGCAGGAATGACAAAGCTGCTTTCTGCTAT 1744
QY 1741 GTTCTAGGTGATTTGCTGCTTTTACTGTTATATTAATTTGCCAATATAAGTAATATAGAT 1800
Db 1745 GTTCTAGGTGATTTGCTGCTTTTACTGTTATATTAATTTGCCAATATAAGTAATATAGAT 1804
QY 1801 TATATATGTATAGTTTTCACAAAGCTTAGACCTTTACCTTCCAGGCCACCCACAGTCT 1860
Db 1805 TATATATGTATAGTTTTCACAAAGCTTAGACCTTTACCTTCCAGGCCACCCACAGTCT 1864
QY 1861 TGATATTTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAGCAGATGAAGTAA 1920
Db 1865 TGATATTTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAGCAGATGAAGTAA 1924

QY 1921 GAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAATGCCACACATAGA 1980
Db 1925 GAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAATGCCACACATAGA 1984
QY 1981 ACTCCAAACACATCAATTTCAATTCACAGACTGAGCTGTAGTTAATTTTGTACAGAACT 2040
Db 1985 ACTCCAAACACATCAATTTCAATTCACAGACTGAGCTGTAGTTAATTTTGTACAGAACT 2044
QY 2041 ATGACTGAATCTAATGCTTCCAAAAATGTTGTTTGGTTCAAAAATATCAAAACATTTGTTAT 2100
Db 2045 ATGACTGAATCTAATGCTTCCAAAAATGTTGTTTGGTTCAAAAATATCAAAACATTTGTTAT 2104
QY 2101 GCAAGAAATTAATTAATTAACAAAATGAAGATTATACCATTTGTTTAAAGCTGACTGAA 2160
Db 2105 GCAAGAAATTAATTAATTAACAAAATGAAGATTATACCATTTGTTTAAAGCTGACTGAA 2164
QY 2161 CTAATCTGTGGAATGCAATGCTGAACTGTAAAGCAAGTATCAATAAAGCTTATAGACT 2220
Db 2165 CTAATCTGTGGAATGCAATGCTGAACTGTAAAGCAAGTATCAATAAAGCTTATAGACT 2224
QY 2221 TAAAAAATAA 2231
Db 2225 TAAAAAATAA 2235
RESULT 3
ABK90133
ID ABK90133 standard; DNA; 2052 BP.
XX AC ABK90133;
XX DT 21-OCT-2002 (first entry)
XX DE DNA encoding human NogoB protein.
XX KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW tissue hypertrophy; central nervous system; axon regeneration; NogoB;
KW Nogo-associated disease; metastasis; gene; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
CDS 67..1188
FT /*tag= a
FT /product= "Human NogoB protein"
XX WO200257483-A2.
XX PD 25-JUL-2002.
XX PF 18-JAN-2002; 2002WO-GB000228.
XX PR 18-JAN-2001; 2001GB-00001312.
XX PA (GLAX) GLAXO GROUP LTD.
XX PA (SMIK) SMITHKLINE BEECHAM PLC.
XX PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
XX WPI; 2002-599722/64.
XX P-PSDB; ABG30937.
XX PT Identifying modulators of Nogo or BACE activity for treating acute
XX neuronal injuries, neoplastic or dysproliferative disorders, comprises
XX providing and monitoring interaction between Nogo and BACE polypeptides.
XX PS Disclosure; Page 50-52; 68pp; English.
XX CC The present invention relates to a new method of identifying modulators
of Nogo function or BACE activity. The method involves providing Nogo and

Qy	1866	TTTCAGAGTCAGTCATTTGGTTATACATGTGTAGTTCTCAAAGCACATTAAGCTTAGAAGA	1925
Db	1700	TTTCAGAGTCAGTCATTTGGTTATACATGTGTAGTTCTCAAAGCACATTAAGCTTAGAAGA	1759
Qy	1926	AATATTCTTAGGAGCACTACCATCTGTTTTCACATCAATGAATGCCACACACATAGACTCC	1985
Db	1760	AATATTCTTAGGAGCACTACCATCTGTTTTCACATCAATGAATGCCACACATAGACTC-	1818
Qy	1986	AACAACATCAATTTTCATTGTCACAGACTGACTGTAGTTAAATTTTGTCA CAGAATCTATGGA	2045
Db	1819	--CAACATCAATTTTCATTGTCACAGACTGACTGTAGTTAAATTTTGTCA CAGAATCTATGGA	1876
Qy	2046	CTGAATCTAATGCTTCCAAAATGTTGTTTGTGCAAAATATCAAAATTTGTTATGCAAG	2105
Db	1877	CTGAATCTAATGCTTCCAAAATGTTGTTTGTGCAAAATATCAAAATTTGTTATGCAAG	1936
Qy	2106	AAATTTAATTAACAAAATGAAGATTTATACCATTTGTGGTTTAAAGCTGTACTGAACTAAA	2165
Db	1937	AAATTTAATTAACAAAATGAAGATTTATACCATTTGTGGTTTAAAGCTGTACTGAACTAAA	1996
Qy	2166	TCGTGGAATGCATTTGTGAACCTGTAAAGCAAGATATCAATTAAGCTTTATAGACTT	2221
Db	1997	TCGTGGAATGCATTTGTGAACCTGTAAAGCAAGATATCAATTAAGCTTTATAGACTT	2052

RESULT 4
AAZ36230
ID AAZ36230 standard; cDNA; 1610 BP.
XX
XX AAZ36230;
XX AC
XX DT 22-FEB-2000 (first entry)
XX
XX cDNA encoding a bone marrow secreted protein designated BMS112.
XX
XX Bone marrow secreted protein; bone marrow stromal cell; cytokine;
XX cell proliferation; cell differentiation; hematopoiesis; anaemia;
XX myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
XX erythroid progenitor cell; colony stimulating factor; granulocyte;
XX monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
XX platelet disorder; thrombocytopenia; hematopoietic stem cell;
XX stem cell disorder; aplastic anaemia; bone differentiation;
XX paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
XX ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
XX bone fracture; cartilage damage; artificial joint; ss.

Accession	Gene	Protein	Location/Qualifiers
AA014266	CD5	CD5	132..1253
AA014267	CD5	CD5	/*tag= a
AA014268	CD5	CD5	/product= "bone marrow secreted protein"
AA014269	CD5	CD5	1516..1521
AA014270	CD5	CD5	/*tag= b

PN	WO9933979-A2.
XX	
XX	
PD	08-JUL-1999.
XX	
PF	18-DEC-1998; 98WO-US027008.
XX	
PR	30-DEC-1997; 97US-0068958P.
PR	24-SEP-1998; 98US-0101603P.
PR	30-SEP-1998; 98US-0102540P.
XX	
PA	(CHIR) CHIRON CORP.
XX	
PI	Lin H, Cao L;
XX	
DR	WPI; 2000-038344/03.
DR	P-PSDB; AAY53624.
XX	

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|||||
Db 541 ACAGAGCTCCGGCCCGGCTCCCTCTCTCCCGGCGAGGCTGAGCCCCCAGGCGAGC 600
Qy 607 CCGTGTGGAACCCCGCCAGCCCGGCTCCCGCGCGCGCCCCCTCCACCCCGCGCGCCCA 666
Db 601 CCGTGTGGAACCCCGCCAGCCCGGCTCCCGCGCGCGCCCCCTCCACCCCGCGCGCCCA 660
Qy 667 AGCGAGGGGCTCTCCGGGCTCAGTGTGTGTGACCTCTGTACTGAGAGACATTAAGA 726
Db 661 AGCGAGGGGCTCTCCGGGCTCAGTGTGTGTGACCTCTGTACTGAGAGACATTAAGA 720
Qy 727 AGACTGAGTGGTGTGTGGTCCAGCCTATTCCTGTGCTTTCATTCAGACATTTACGA 786
Db 721 AGACTGAGTGGTGTGTGGTCCAGCCTATTCCTGTGCTTTCATTCAGACATTTACGA 780
Qy 787 TTGTGAGCGTAAACGCTACATTCCTGTGCGCTCTCTGTGACCATCAGCTTTAGGA 846
Db 781 TTGTGAGCGTAAACGCTACATTCCTGTGCGCTCTCTGTGACCATCAGCTTTAGGA 840
Qy 847 TATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCAT 906
Db 841 TATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCAT 900
Qy 907 ATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGATCAGATAATCTGCTC 966
Db 901 ATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGATCAGATAATCTGCTC 960
Qy 967 TTGGTCAATGGAACGCAAGATAAGGAACCTCAGGCGCTCTCTTAGTTGATGATTTAG 1026
Db 961 TTGGTCAATGGAACGCAAGATAAGGAACCTCAGGCGCTCTCTTAGTTGATGATTTAG 1020
Qy 1027 TTGATTTCTGAAGTTGCGAGTGTGATGGGGTATTTACCTATGTTGGTCCCTGTTTAA 1086
Db 1021 TTGATTTCTGAAGTTGCGAGTGTGATGGGGTATTTACCTATGTTGGTCCCTGTTTAA 1080
Qy 1087 ATGCTCTGACACTACTGATTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATG 1146
Db 1081 ATGCTCTGACACTACTGATTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATG 1140
Qy 1147 AACGGCATCAGGCACAGATAGATCAATTCATGAGACTTGCATAAAGATGTTAAAGATG 1206
Db 1141 AACGGCATCAGGCACAGATAGATCAATTCATGAGACTTGCATAAAGATGTTAAAGATG 1200
Qy 1207 CTATGGCTAAATCAAGCAAAAATCCCTGATTTGAAGCGCAAAAGCTGAATGAAACGCC 1266
Db 1201 CTATGGCTAAATCAAGCAAAAATCCCTGATTTGAAGCGCAAAAGCTGAATGAAACGCC 1260
Qy 1267 CAAATTAATAGTAGGAGTTTCATCTTTAAAGGGATATTCATTTGATTATACGGGGAGG 1326
Db 1261 CAAATTAATAGTAGGAGTTTCATCTTTAAAGGGATATTCATTTGATTATACGGGGAGG 1320
Qy 1327 GTCAGGGAAGAAACGAACCTTGACGTTGCGAGTGCAGTTCAGATCGTTGTTAGATCTTT 1386
Db 1321 GTCAGGGAAGAAACGAACCTTGACGTTGCGAGTGCAGTTCAGATCGTTGTTAGATCTTT 1380
Qy 1387 ATTTTTCAGCATGACCTGTTGTGAGGAAAAATACCTGTCTTGATGTCATGCTTCATC 1446
Db 1381 ATTTTTCAGCATGACCTGTTGTGAGGAAAAATACCTGTCTTGATGTCATGCTTCATC 1440
Qy 1447 ATCTTAAGTATTTAAGCTGTATGATGATTTTAAACCGTAAATCATATCTTTTCTTAT 1506
Db 1441 ATCTTAAGTATTTAAGCTGTATGATGATTTTAAACCGTAAATCATATCTTTTCTTAT 1500
Qy 1507 CTGAGGCATCTGGTGGAAATAAAAAACCTGTATATTTTACTTTGTTGCGAGATGCTTCGCG 1566
Db 1501 CTGAGGCATCTGGTGGAAATAAAAAACCTGTATATTTTACTTTGTTGCGAGATGCTTCGCG 1560
Qy 1567 CATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAATAAAAAA 1615
Db 1561 CATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAATAAAAAA 1609
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RESULT 5

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AAK94408
ID AAK94408 standard; cDNA; 1694 BP.
XX
AC AAK94408;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human full-length cDNA, SEQ ID NO: 3170.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; es.
XX
OS Homo sapiens.
XX
PN EF1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
(HELI-) HELIX RES INST.
XX
PA Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
DR WPI; 2001-524255/58.
DR P-PSDB; AAM93484.
XX
830 Primers useful for synthesizing full length cDNA clones and their use
in genetic manipulation.
Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.
XX
The invention relates to primers for synthesising full length cDNA
clones. 830 cDNA molecules encoding a human protein have been isolated
and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have
been determined. Primers for synthesising the full length cDNA are useful
for clarifying the function of the protein encoded by the cDNA. The full
length clones were obtained by construction of full length enriched cDNA
libraries that were synthesised by the oligo-capping method. The primers
enable the production of the full length cDNA easily without any special
methods. The present sequence is a full length human cDNA of the
invention. Note: The sequence data for this patent did not form part of
the printed specification, but was obtained in CD-ROM format directly
from EPO
XX
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
Query Match 70.8%; Score 1586.4; DB 4; Length 1694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1598; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CGTCACACAGTAGTGGTCCCTCGGCTCAGTCGGCCAGCCCTCTTCAGTCTCCCAACCC 60
Db 95 CGTCACACAGTAGTGGTCCCTCGGCTCAGTCGGCCAGCCCTCTTCAGTCTCCCAACCC 154
Qy 61 CCACACCGCCCGCGCTCTGAGACCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 155 CCACACCGCCCGCGCTCTGAGACCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 214
Qy 121 ATCTCCACCTCTCAGCCATCGAAGACCTGGAACAGTCTCTCTGGTCTCGTCTCGGACA 180
Db 215 ATCTCCACCTCTCAGCCATCGAAGACCTGGAACAGTCTCTCTGGTCTCGTCTCGGACA 274
Qy 181 GCCCACCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 275 GCCCACCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 334
Qy 241 AGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
|||||
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QY 1 CGTCACACAGTAGTCCCTGGCTCAGTCGGCCAGCCCTCTCAGTCTCTCCCAACC 60
Db |||||
QY 95 CGTCACACAGTAGTCCCTGGCTCAGTCGGCCAGCCCTCTCAGTCTCTCCCAACC 154
Db |||||
QY 61 CCACAAACCGCCCGGCTCTGAGACGGCCCGCGCGCGCGCAGCAGCTGCAGCATC 120
Db |||||
QY 155 CCACAAACCGCCCGGCTCTGAGACGGCCCGCGCGCGCGCAGCAGCTGCAGCATC 214
Db |||||
QY 121 ATCTCCACCTCTCAGCCATGGAAGACCTGAGACAGTCTCTCTGGTCTCTGCTCTCGGACA 180
Db |||||
QY 215 ATCTCCACCTCTCAGCCATGGAAGACCTGAGACAGTCTCTCTGGTCTCTGCTCTCGGACA 274
Db |||||
QY 181 GCCCACCCCGCCGACCGCCGCTTCAAGTACCAAGTTCGTGAGGGAGCCGAGAGCAGG 240
Db |||||
QY 275 GCCCACCCCGCCGACCGCCGCTTCAAGTACCAAGTTCGTGAGGGAGCCGAGAGCAGG 334
Db |||||
QY 241 AGGAAGAGAGGAGGAGAGAGAGAGACGAGAGACGAAGACCTGAGGAGCTGAGGTGC 300
Db |||||
QY 335 AGGAAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGC 394
Db |||||
QY 301 TGGAGAGGAAGCCCGCCCGGCTGTCCGCGGCCCGCAGTGCCCAACCGCCCTTGCOCGCG 360
Db |||||
QY 395 TGGAGAGGAAGCCCGCCCGGCTGTCCGCGGCCCGCAGTGCCCAACCGCCCTTGCOCGCG 454
Db |||||
QY 361 GCGGCGCCCTGATGGAATCTTGGAAATGACTTCTGTCGCGCGCGCGCCCGGGAGCCCTGC 420
Db |||||
QY 455 GCGGCGCCCTGATGGAATCTTGGAAATGACTTCTGTCGCGCGCGCGCCCGGGAGCCCTGC 514
Db |||||
QY 421 CGGCGCTCTCCCGCG - TCGCCCGCGGAGCGGAGCGCTTGGAGACCGAGCGCGTCTCG 479
Db |||||
QY 515 CGGCGCTCTCCCGCGTTCGCCCCGAGCGGAGCGGAGCGCTTGGAGACCGAGCGCGGTGCG 574
Db |||||
QY 480 TCGACCGTCTCCCGCCATCCCGCTGTCTGTCGCGCAGTCTCGCCCTCCAAAGCTCCCT 539
Db |||||
QY 575 TCGACCGTCTCCCGCCATCCCGCTGTCTGTCGCGCAGTCTCGCCCTCCAAAGCTCCCT 634
Db |||||
QY 540 GAGAGACAGAGCTCGCGCGCGGCTCCCGCTCTCTCCCGCGGCGAGGTGAGCCCGCAG 599
Db |||||
QY 635 GAGAGACAGAGCTCGCGCGCGGCTCCCGCTCTCTCCCGCGGCGAGGTGAGCCCGCAG 694
Db |||||
QY 600 GCAGAGCCCGTGTGAGCCCGCGAGCCCGGCTCCCGCGCGGCGGCTCCACCCCGGCG 659
Db |||||
QY 695 GCAGAGCCCGTGTGAGCCCGCGAGCCCGGCTCCCGCGCGGCGGCTCCACCCCGGCG 754
Db |||||
QY 660 GCGCCCAAGCGCAGGGGCTCTCGGGCTCAGTGGTGTGACCTCTCTGTACTGGAGAGAC 719
Db |||||
QY 755 GCGCCCAAGCGCAGGGGCTCTCGGGCTCAGTGGTGTGACCTCTCTGTACTGGAGAGAC 814
Db |||||
QY 720 ATTAAGAGACTGAGTGGTGTGGTGGCCAGCCCTATCTCTGCTGCTTTTCAATGACAGTA 779
Db |||||
QY 815 ATTAAGAGACTGAGTGGTGTGGTGGTGTGAGCCCTATCTCTGCTGCTTTTCAATGACAGTA 874
Db |||||
QY 780 TTAGCATTGTGAGCTTAACAGCTTACATGTCCTGGCCCTGCTCTGTGACCATCAGC 839
Db |||||
QY 875 TTAGCATTGTGAGCTTAACAGCTTACATGTCCTGGCCCTGCTCTGTGACCATCAGC 934
Db |||||
QY 840 TTTAGGATATACAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCATTC 899
Db |||||
QY 935 TTTAGGATATACAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCATTC 994
Db |||||
QY 900 AGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAATACAGTAAT 959
Db |||||
QY 995 AGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAATACAGTAAT 1054
Db |||||
QY 960 TCTGCTCTTGTGCTATGTAAGTCAAGTCAAGTAAAGAACTCAGGCGGCTCTTCTAGTTGAT 1019
Db |||||
QY 1055 TCTGCTCTTGTGCTATGTAAGTCAAGTCAAGTAAAGAACTCAGGCGGCTCTTCTAGTTGAT 1114
Db |||||
QY 1020 GATTAGTGTGATCTCTGAAGTTTGCAGTGTGTGATGGGTATTTACTATGTTGGTGCC 1079
Db |||||
QY 1115 GATTAGTGTGATCTCTGAAGTTTGCAGTGTGTGATGGGTATTTACTATGTTGGTGCC 1174
Db |||||
QY 1080 TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCAATTTTCACTCTTTCAGTGTTCCTGTT 1139
Db |||||
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Db |||||
QY 1175 TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCAATTTCACTCTTCAGTGTCCCTGTT 1234
Db |||||
QY 1140 ATTTATGAACGGCATCAGGCACAGATAGATCAATTTATCTAGGACTTGCAATAAGAATGTT 1199
Db |||||
QY 1235 ATTTATGAACGGCATCAGGCACAGATAGATCAATTTATCTAGGACTTGCAATAAGAATGTT 1294
Db |||||
QY 1200 AAGATGCTATGCTTAAATCCAAAGCAAAATCCCTGGATTTGAAGCGCAAGCTGAATGA 1259
Db |||||
QY 1295 AAGATGCTATGCTTAAATCCAAAGCAAAATCCCTGGATTTGAAGCGCAAGCTGAATGA 1354
Db |||||
QY 1260 AAACGCCCAAAATAATTTAGTAGGAGTTTCATCTTTAAAGGGGATATTCAATTTGATTATACG 1319
Db |||||
QY 1355 AAACGCCCAAAATAATTTAGTAGGAGTTTCATCTTTAAAGGGGATATTCAATTTGATTATACG 1414
Db |||||
QY 1320 GGGGAGGGTCTAGGGAAGAACGAACCTTTGACGTTTGCAGTGCAGTTTTCACAGATCGTTGTTA 1379
Db |||||
QY 1415 GGGGAGGGTCTAGGGAAGAACGAACCTTTGACGTTTGCAGTGCAGTTTTCACAGATCGTTGTTA 1474
Db |||||
QY 1380 GATCTTTATTTTGTAGCCATGCACCTGTTGTGAGGAAATTAACCTTCTTGCATGCCATGT 1439
Db |||||
QY 1475 GATCTTTATTTTGTAGCCATGCACCTGTTGTGAGGAAATTAACCTTCTTGCATGCCATGT 1534
Db |||||
QY 1440 GTTCATCATCTTAAGTATTTGTAAGCTGCTATGATGATGATTTAAACCTTAATCATATCTTT 1499
Db |||||
QY 1535 GTTCATCATCTTAAGTATTTGTAAGCTGCTATGATGATGATTTAAACCTTAATCATATCTTT 1594
Db |||||
QY 1500 TTCTTATCTCAGGCACCTGGTGGAAATAAAAACCTGTATATTTTACTTTTGTGAGATAGT 1559
Db |||||
QY 1595 TTCTTATCTCAGGCACCTGGTGGAAATAAAAACCTGTATATTTTACTTTTGTGAGATAGT 1654
Db |||||
QY 1560 CTTCGCGCATCTTGGCAAGTTGCGAGATGCGTGAGCTAG 1599
Db |||||
QY 1655 CTTCGCGCATCTTGGCAAGTTGCGAGATGCGTGAGCTAG 1694
Db |||||
```

RESULT 7

AAF32725/c
ID AAF32725 standard; cDNA; 1758 BP.

AC AAF32725;

XX 23-MAR-2001 (first entry)

XX Human secreted protein gene 27 SEQ ID NO:37.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; neutropenic; neuroprotective; antibacterial; virucide;
XX fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
XX cardiac arrest; cerebrovascular disorder; cerebral ischaemia; infection;
XX angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;
XX ocular disorder; corneal infection; wound healing; food additive;
XX preservative; ss.

XX Homo sapiens.

XX WO200077255-A1.

XX 21-DEC-2000.

XX 01-JUN-2000; 2000MO-US014926.

XX 11-JUN-1999; 99US-0138628P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis GA;

XX WPI; 2001-025337/03.

XX P-PSDB; AAB64448.

XX

PT Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.

The polynucleotide sequences given in AAF32699 to AAF32747 encode the human secreted proteins given in AAB64422 to AAB64470. AAB64471 to AAB64548 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAF32690 to AAF32698 and AAB64421 represent sequences used in the exemplification of the present invention

Sequence 1758 BP; 524 A; 380 C; 348 G; 504 T; 0 U; 2 Other;

Query Match	70.6%;	Score 1581;	DB 4;	Length 1758;
Best Local Similarity	96.5%;	Pred. No. 0;		
Matches 1661;	Conservative 0;	Mismatches 0;	Indels 60;	Gaps 2;
QY	577	CCCCGGCCAGCGTCAGCCGCCCCAGACGAGCCCGTGTGACCCCGCCAGCCCGCGCTCCCG	636	
Db	1750	CCCCGGCCAGCGGTGAGCCCCCAGACGAGCCCGTGTGACCCCGCCAGCCCGCGCTCCCG	1691	
QY	637	CCGCGCCCCCCTTCCACCCCGGCCCGCCCAAGCGCAGCGGGCTCTCGGGCTCAGTG----	692	
Db	1690	CCGCGCCCCCCTTCCACCCCGGCCCGCCCAAGCGCAGCGGGCTCTCGGGCTCAGTGGATG	1631	
QY	693	-----GTTCTGTG	699	
Db	1630	AGACCCCTTTTGTCTTCTGCTCGATCTGAGCCTGTGATACGCTCTCTGCGAGTGTGTG	1571	
QY	700	ACCTCTCTGTACTGAGAGACATTAAGAAAGACTGAGAGTGGTGTTTGGTGCCAGACCTATTCC	759	
Db	1570	ACCTCTCTGTACTGAGAGACATTAAGAAAGACTGAGAGTGGTGTTTGGTGCCAGACCTATTCC	1511	
QY	760	TGTCGCTTTCAATTGACAGTATTCAGCATTTGACCGTAAACGCTCAATTCGCTTTGGCCC	819	
Db	1510	TGTCGCTTTCAATTGACAGTATTCAGCATTTGACCGTAAACGCTCAATTCGCTTTGGCCC	1451	
QY	820	TGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAGAGCTATCCAGAAAT	879	
Db	1450	TGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAGAGCTATCCAGAAAT	1391	
QY	880	CAGATGAAGGCCACCCATTCAGGCCATATCTGGAAATCTGAAGTTGCTATATCTCAGGAGT	939	
Db	1390	CAGATGAAGGCCACCCATTCAGGCCATATCTGGAAATCTGAAGTTGCTATATCTCAGGAGT	1331	
QY	940	TGGTTTCAGAGGTACAGTAATTTCTGCTCTTGTCATGTGAACCTGCACCGATAAAGAACTCA	999	
Db	1330	TGGTTTCAGAGGTACAGTAATTTCTGCTCTTGTCATGTGAACCTGCACCGATAAAGAACTCA	1271	
QY	1000	GGCGCCTCTTCTTAGTTAGTGATTTAGTTAGTTCTCTGAAGTTTGCAGTGTGTGATGTGGG	1059	

Qy 2140 TGTGGTTAAAGCTGACTGAACCTAAATCTGTGGAATGCAATGTGAACCTGTAAGAGAAAG 2199
Db 133 TGTGGTTAAAGCTGACTGAACCTAAATCTGTGGAATGCAATGTGAACCTGTAAGAGCAAG 74
Qy 2200 TATCAATAAAGCTTATAGACTTAAATAAAAAAAAAAAAAAAAAAAAAA 2240
Db 73 TATCAATAAAGCTTATAGACTTAAATAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 8

ID ADI62860 standard; cDNA; 1599 BP.
XX ADI62860;
XX 22-APR-2004 (first entry)
XX Human apoptosis-associated cDNA SEQ ID 303.
XX apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
KW anti-rheumatic; antiarthritic; dermatological; anti-inflammatory;
KW hepatotropic; virucide; nontropic; anticonvulsant; antiparkinsonian;
KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;
KW autoimmune disease; degenerative disease; viral infection; leukaemia;
KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
KW lupus; hepatitis; influenza viruses; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; reperfusion injury; stroke;
KW alcoholic liver disease; human; gene; ss.

XX Homo sapiens.

XX WO2003058021-A2.

XX 17-JUL-2003.

XX 13-JAN-2003; 2003WO-EP000270.

XX 11-JAN-2002; 2002DE-01000856.

XX (XANT-) XANTOS BIOMEDICINE AG.

XX Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;

XX WPI; 2003-542134/51.

XX New nucleic acids involved in apoptosis, useful for diagnosis and
PT treatment of e.g. tumors and degenerative disease, also related proteins,
PT antibodies and modulators.

XX Claim 1b; SEQ ID NO 303; 517bp; German.

XX This invention describes novel nucleic acid molecules that are associated
CC with apoptosis and encode a polypeptide and are derived from a normalised
CC gene library (embryonic or liver) or clone collections, and the extent of
CC apoptosis measured by cell death detection assay or the CPRG assay
CC (measuring loss of membrane integrity). The products of the invention
CC have cytostatic, neuroprotective, immunosuppressive, antirheumatic,
CC antiarthritic, dermatological, anti-inflammatory, hepatotropic, virucide,
CC nontropic, anticonvulsant, antiparkinsonian, vasotropic,
CC cerebroprotective and antialcoholic activity and can be used for gene
CC therapy. The polynucleotides also related vectors, hosts (or their
CC extracts), encoded polypeptide (or their receptors) and/or agents that
CC inhibit their activity (including antisense sequences) are used for
CC treatment or prevention of tumours, autoimmune or degenerative diseases
CC and viral infections, specifically leukaemia, carcinoma, sarcoma,
CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection
CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or
CC Parkinson's disease, reperfusion injury, stroke and alcoholic liver
CC disease. Detection of the polynucleotides and derived polypeptides can
CC also be used for diagnosis of these diseases. This sequence encodes an
CC apoptosis-associated protein described in the disclosure of the
CC invention.

XX SQ Sequence 1599 BP; 354 A; 452 C; 422 G; 371 T; 0 U; 0 Other;
Query Match 70.4%; Score 1577.4; DB 10; Length 1599;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1592; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
Qy 23 GCTCAGTCGGCCAGCCCTCTCAGTCTCTCCCAACCCCAACCCCGCGCTCTGA 82
Db 1 GCTCAGTCGGCCAGCCCTCTCAGTCTCTCCCAACCCCAACCCCGCGCTCTGA 60
Qy 83 GACGCGCCCGCGCGCGGCGAGCAGCTGCAGCATCATCTCCACCCCTCCAGCATGGA 142
Db 61 GACGCGCCCGCGCGCGGCGGCGAGCAGCTGCAGCATCATCTCCACCCCTCCAGCATGGA 120
Qy 143 AGACCTGGACCAAGTCTCTCTGTCTCTGGTCTCGGACAGCCCAACCCCGCGCGCATGCCG 202
Db 121 AGACCTGGACCAAGTCTCTCTGTCTCTGTCTCTCGGACAGCCCAACCCCGCGCGCATGCCG 180
Qy 203 GTTCAAGTACCAAGTCTGTGAGGAGCCCGGAGGAGGAGGAGGAGGAGGAAGA 262
Db 181 GTTCAAGTACCAAGTCTGTGAGGAGCCCGGAGGAGGAGGAGGAGGAGGAAGA 240
Qy 263 GGAGGACGAGGACGAGACCTCGAGGAGCTGGAGGTCTCTGAGAGGAAGCCCGCGCGG 322
Db 241 GGAGGACGAGGACGAGACCTCGAGGAGCTGGAGGTCTCTGAGAGGAAGCCCGCGCGG 300
Qy 323 GCTGTCTCGCGCGCCCAAGTGCCTCCAGCCCTGCGCGCGCGCGCTCTGATGACTTCGG 382
Db 301 GCTGTCTCGCGCGCCCAAGTGCCTCCAGCCCTGCGCGCGCGCGCTCTGATGACTTCGG 360
Qy 383 AAATGACTTCTGTCGCGCGCGCGCGCGGAGACCCCTGTCGCGCGCGCTCCCCCGTGCGCC 442
Db 361 AAATGACTTCTGTCGCGCGCGCGCGCGGAGACCCCTGTCGCGCGCGCTCCCCCGTGCGCC 420
Qy 443 GGAGCGGACAGCGCTCTTGGGACCGGAGCCGCGCTGTCGACCGTGCAGCGCGCGCATCCCC 502
Db 421 GGAGCGGACAGCGCTCTTGGGACCGGAGCCGCGGTGTCGTCGACCGTGCAGCGCGCATCCCC 480
Qy 503 GCTGTCTGTCGCGCGAGTCTCGCCCTCCAAAGCTCCCTGAGGAGACGACGAGCTCCGCGCGG 562
Db 481 GCTGTCTGTCGCGCGAGTCTCGCCCTCCAAAGCTCCCTGAGGAGACGACGAGCTCCGCGCGG 540
Qy 563 GCTTCCCGCTCTCTCCCGCGCGAGCGTGAAGCCCGCGCGAGAGCCCTGTGGAACCCCGCG 622
Db 541 GCCTCCCGCTCTCTCCCGCGCGAGCGTGAAGCCCGCGCGAGAGCCCTGTGGAACCCCGCG 600
Qy 623 AGCCCGGCTCCCGCGCGCGCGCGCTCCACCCCGCGCGCGCGCCCAAGCGCAGGGGCTCCTC 682
Db 601 AGCCCGGCTCCCGCGCGCGCGCGCTCCACCCCGCGCGCGCGCCCAAGCGCAGGGGCTCCTC 660
Qy 683 GGGCTCAGTGGTGTGACCTCTCTGTACTGGAGAGACATTAAGAAAGACTGGAGTGGTGT 742
Db 661 GGGCTCAGTGGTGTGACCTCTCTGTACTGGAGAGACATTAAGAAAGACTGGAGTGGTGT 720
Qy 743 TGTGTCAGGCTATTCTCTGCTCTTTCATTGACAGTATTGAGCATTGTGAGCGTAAACAGC 802
Db 721 TGTGTCAGGCTATTCTCTGCTCTTTCATTGACAGTATTGAGCATTGTGAGCGTAAACAGC 780
Qy 803 CTACATTGCTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGAT 862
Db 781 CTACATTGCTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGAT 840
Qy 863 CCAAGCTATCCAGAAATCAGATCAAGGCCACCCATTCAGGGGCATATCTGGAATCTGAAGT 922
Db 841 CCAAGCTATCCAGAAATCAGATCAAGGCCACCCATTCAGGGGCATATCTGGAATCTGAAGT 900
Qy 923 TGCTATATCTGAGGAGTGGTTTCAGAGATACAGTAATTTCTGGTCTCATGTGAACCTG 982
Db 901 TGCTATATCTGAGGAGTGGTTTCAGAGATACAGTAATTTCTGGTCTCATGTGAACCTG 960
Qy 983 CAGCATAAAGGAACCTCAGGCGCTCTTCTAGTTGATGATTTAGTTCTCTGGAATTT 1042

Dd 961 CACGATAAAGGAACCTACGGCGCCTCTTCTTAGTGTGATGATTTAGTGTGATTTCTCTGAAAGTT 1020
Qy 1043 TGCAGTGTGTAGTGGGTATTTACCTATGTTGGTGCCTTGTATATGCTCTGACACTACT 1102
Dd 1021 TGCAGTGTGTAGTGGGTATTTACCTATGTTGGTGCCTTGTATATGCTCTGACACTACT 1080
Qy 1103 GATTTTGGCTCTCATTTTCACTCTTCAGTGTGCTCTTATTTATGAAACGGCATCAGGCACA 1162
Dd 1081 GATTTTGGCTCTCATTTTCACTCTTCAGTGTGCTCTTATTTATGAAACGGCATCAGGCACA 1140
Qy 1163 GATAGATCATTTATCTAGGACTTGCAAAATGAAGTGTAAAGTGTATGCTGTAAATCCA 1222
Dd 1141 GATAGATCATTTATCTAGGACTTGCAAAATGAAGTGTAAAGTGTATGCTGTAAATCCA 1200
Qy 1223 AGCAAAAATCCCTGATTTCAAGCGCAAGAGCTGAATGAAAAAGCCCAAAATAATTAGTAGG 1282
Dd 1201 AGCAAAAATCCCTGATTTGAAGCGCAAGAGCTGAATGAAAAAGCCCAAAATAATTAGTAGG 1260
Qy 1283 AGTTCATCTTTAAAGGGGATATTCATTTGATTTATACGGGGGAGGTCAGGGAAGAACGAA 1342
Dd 1261 AGTTCATCTTTAAAGGGGATATTCATTTGATTTATACGGGGGAGGTCAGGGAAGAACGAA 1320
Qy 1343 CTTTGACGTTGACGTGACGTTTCACAGATCGTTGTAGATCTTTATTTTATGCCATGAC 1402
Dd 1321 CTTTGACGTTGACGTGACGTTTCACAGATCGTTGTAGATCTTTATTTTATGCCATGAC 1380
Qy 1403 TGTGTGAGGAAAAATACCTGTCTTGTGCTGATGTCATCATCTTTAAAGTATTGTA 1462
Dd 1381 TGTGTGAGGAAAAATACCTGTCTTGTGCTGATGTCATCATCTTTAAAGTATTGTA 1440
Qy 1463 GCTGCTATGTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGG 1518
Dd 1441 GCTGCTATGTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACTGG 1500
Qy 1519 TGGATAAATAAACCTGTATATTTTACTTTTGTGACATAGTCTTGCCGCATCTTGGCAAG 1578
Dd 1501 TGGATAAATAAACCTGTATATTTTACTTTTGTGACATAGTCTTGCCGCATCTTGGCAAG 1560
Qy 1579 TTGCAGAGATGGTGAGCTAGAAAAAAGAAAAA 1615
Dd 1561 TTGCAGAGATGGTGAGCTAGAAAAAAGAAAAA 1597

RESULT 9
ADR83534
ID ADR83534 standard; DNA; 4789 BP.
XX
AC ADR83534;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human reticulon 4 DNA, target gene of miRNA.
XX
KW human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;
KW immune disease; nerve disorder; amyotrophic lateral sclerosis;
KW Parkinson's disease; Alzheimer's disease; inflammatory disease;
KW siRNA silencing precursor; cytostatic; immunosuppressive; neurotropic;
KW neuroprotective; antiinflammatory; immunotherapy; reticulon 4.
XX
OS Homo sapiens.
XX
PN WO2004076622-A2.
XX
PD 10-SEP-2004.
XX
PF 10-FEB-2004; 2004WO-JP001433.
XX
PR 10-FEB-2003; 2003US-0445829P.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PI Taira K, Kawasaki H;
XX

DR WPI; 2004-653393/63.
XX
PT Modulating expression of a target gene in a cell, for treating cancer, an
PT immune disease, or a nerve disorder, comprises introducing into the cell
PT a polynucleotide that forms a duplex region with an mRNA transcribed from
PT the target gene.
XX
PS Claim 9; SEQ ID NO 436; 865pp; English.
XX
CC This invention relates to a novel method for modulating the expression of
CC a target gene in a cell. Specifically, it refers to the introduction into
CC a cell of a polynucleotide that forms a duplex region with an mRNA
CC transcribed from the target gene, where the duplex region comprises a
CC mammalian mRNA target region i.e. a non-coding microRNA (miRNA) that
CC regulates mRNA at a post-transcriptional level. The present invention
CC describes a method for controlling ontogenesis of a mammal, function of a
CC mammalian cell, differentiation of a mammalian cell or viability of a
CC mammalian cell in the post-transcriptional phase, which comprises
CC introducing a plasmid vector comprising a promoter and nucleic acid
CC molecule expressing an miRNA or siRNA silencing precursor to the miRNA.
CC Accordingly, it provides a cell therapy method for treating cancer,
CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,
CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease
CC by introducing into the cell the miRNA, siRNA silencing precursor to the
CC miRNA or the plasmid vector. As such, they can be developed into
CC pharmaceutical compositions that exhibit cytostatic, immunosuppressive,
CC neurotropic, neuroprotective and antiinflammatory activities and hence can
CC be used for immunotherapy. This polynucleotide sequence is a human target
CC gene whose expression is modulated by miRNAs of the invention.
XX
SQ Sequence 4789 BP; 1422 A; 1052 C; 1075 G; 1240 T; 0 U; 0 Other;
Query Match 68.4%; Score 1533; DB 13; Length 4789;
Best Local Similarity 100.0%; Pred. No. 1.1e-309;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 693 GTTGTGACCTCTGTACTGGAGAGACATTAAAGAAGCTGGAGTGGTGTGGTGGCCAGC 752
Dd 3257 GTTGTGACCTCTGTACTGGAGAGACATTAAAGAAGCTGGAGTGGTGTGGTGGCCAGC 3316
Qy 753 CTATTCCTGCTGCTTTCATTGACAGATTTACAGCATTTGACGCTTAACAGCTCATATTGCC 812
Dd 3317 CTATTCCTGCTGCTTTCATTGACAGATTTACAGCATTTGACGCTTAACAGCTCATATTGCC 3376
Qy 813 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCGTGTGATCCAAGCTATC 872
Dd 3377 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCGTGTGATCCAAGCTATC 3436
Qy 873 CAGAAATCAGATGAAGGCCACCCATTTCAGGSCATATCTGGAATCTGAAGTTGCTATATCT 932
Dd 3437 CAGAAATCAGATGAAGGCCACCCATTTCAGGSCATATCTGGAATCTGAAGTTGCTATATCT 3496
Qy 933 GAGAGTTGTTTCAAGAAGTACAGTAATTCGCTCTTGGTCTATGTGAAGTGCACGATAAAG 992
Dd 3497 GAGAGTTGTTTCAAGAAGTACAGTAATTCGCTCTTGGTCTATGTGAAGTGCACGATAAAG 3556
Qy 993 GAACCTCAGGCGCTCTCTTGTAGTGTAGTATTAGTGTATTTCTCTGAAGTTTGCAGTGTG 1052
Dd 3557 GAACCTCAGGCGCTCTCTTGTAGTGTAGTATTAGTGTATTTCTCTGAAGTTTGCAGTGTG 3616
Qy 1053 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGCTCTGACACTACTGATTTGGCT 1112
Dd 3617 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGCTCTGACACTACTGATTTGGCT 3676
Qy 1113 CTCAATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1172
Dd 3677 CTCAATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 3736
Qy 1173 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATTCGAAGCAAAAATC 1232
Dd 3737 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATTCGAAGCAAAAATC 3796
Qy 1233 CCTGGATTGAAGCGCAAAAGCTGAATGAAACGCCCAAAATAATTAGTAGGAGTTCACTTT 1292

Query Match				66.5%; Score 1488.8; DB 6; Length 1798;
Best Local Similarity				99.1%; Pred. No. 1.3e-300;
Matches 1540; Conservative 0; Mismatches 7; Indels 7; Gaps 4;				
Qy	692	GGTTGTTGACCTCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGTGGCAG	751	
Db	247	GGTTGTTGACCTCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGTGGCAG	306	
Qy	752	CCTATTCTGCTGCTTTCATTTGACAGATATTCAGCATTTGAGAGCTTAACAGCTTACATGTC	811	
Db	307	CCTATTCTGCTGCTTTCATTTGACAGATATTCAGCATTTGAGAGCTTAACAGCTTACATGTC	366	
Qy	812	CTTGGCCCTGCTCTCTGCTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTAT	871	
Db	367	CTTGGCCCTGCTCTCTGCTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTAT	426	
Qy	872	CCAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTCGAAGTTGCTATATC	931	
Db	427	CCAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTCGAAGTTGCTATATC	486	
Qy	932	TGAGGAGTTGGTTTCAGAAAGTACAGTAATCTTGGCTCTTGGTCAATGTAACCTGCACGATAAA	991	
Db	487	TGAGGAGTTGGTTTCAGAAAGTACAGTAATCTTGGCTCTTGGTCAATGTAACCTGCACGATAAA	546	
Qy	992	GGAATCAGGCGCCTCTCTTCTAGTTGATGATTTAGTTGATCTCTGAAGTTGCACTGTT	1051	
Db	547	GGAATCAGGCGCCTCTCTTCTAGTTGATGATTTAGTTGATCTCTGAAGTTTGCAGTGT	606	
Qy	1052	GATGTGGTATTTACCTATGTTGGTGGCTGCTTTAATGGTCTGACACTTACTGATTTTGGC	1111	
Db	607	GATGTGGTATTTACCTATGTTGGTGGCTGCTTTAATGGTCTGACACTTACTGATTTTGGC	666	
Qy	1112	TCTCAITTTCACT-CTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATC	1170	
Db	667	TCTCAITTTCACTCTCTCAGTGTCTCTGTTATTTA-GAACGGCATCAGGCACAGATAGATC	725	
Qy	1171	ATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAAA	1230	
Db	726	ATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAAA	785	
Qy	1231	TCCCTGGATTGAAGCGCAAGCTGAAAGAAACGCCCAAAATTAATAGTAGGAGTTTCATC	1290	
Db	786	TCCCTGGATTGAAGCGCAAGCTGAAAGAAACGCCCAAAATTAATAGTAGGAGTTTCATC	845	
Qy	1291	TTTAAAGGGATATTCATTTGATTTATACGGGGAGGGTCAGGGAAGAACCACTTCGACG	1350	
Db	846	TTTAAAGGGATATTCATTTGATTTATACGGGGAGGGTCAGGGAAGAACCACTTCGACG	905	
Qy	1351	TTGAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTACCCATGCACTGTTGTGA	1410	
Db	906	TTGAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTACCCATGCACTGTTGTGA	965	
Qy	1411	GGAAATTTACTGCTCTGACCTGCATGTTGTCATCTTAAAGTATGTAAGCTGCTAT	1470	
Db	966	GGAAATTTACTGCTCTGACCTGCATGTTGTCATCTTAAAGTATGTAAGCTGCTAT	1025	
Qy	1471	GTAATGATTTAAACCGTAATCATATCTTTTTC-CTATCTGAGGCACTGGTGAATAA	1526	
Db	1026	GTAATGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACTGGTGAATAA	1085	
Qy	1527	AAAACCTGTATTTTACTTTGTTGAGATAGTCTTGCCGATCTTTGGCAAGTTGCGAG	1586	
Db	1086	AAAACCTGTATTTTACTTTGTTGAGATAGTCTTGCCGATCTTTGGCAAGTTGCGAG	1145	
Qy	1587	ATGTTGGAGCTAGAAAAAAGAAAAAGCCCTTTTCAGTTTGGCACTGTTGATGGTC	1646	
Db	1146	ATGTTGGAGCTAGAAAAAAGAAAAAGCCCTTTTCAGTTTGGCACTGTTGATGGTC	1205	
Qy	1647	CGTGTAGATTCATGTCAGATTTTCTGAAATGAAATGTTTGTAGACGAGATCATACCGGT	1706	
Db	1206	CGTGTAGATTCATGTCAGATTTTCTGAAATGAAATGTTTGTAGACGAGATCATACCGGT	1265	
Qy	1707	AAAGCAGGAATGACAAAGCTTGTCTTTCTGGTATGTTCTAGGTGTTTGTGACTTTTACT	1766	

Db	1266	AAAGCAGGAATGACAAAGCTTGTCTTCTGGTATGTTCTAGGTGTTTGTGACTTTTACT	1325	
Qy	1767	GTTATATTAATGCTCAATATAAGTAATAATAGATATATATATATATATATATATATATAT	1826	
Db	1326	GTTATATTAATGCTCAATATAAGTAATAATAGATATATATATATATATATATATATATAT	1385	
Qy	1827	TTAGACCTTTACCTTCCAGCCACCCACAGTCTTGTATATTTTCAGAGTCACTTGGTT	1886	
Db	1386	TTAGACCTTTTACCTTCCAGCCACCCACAGTCTTGTATATTTTCAGAGTCACTTGGTT	1445	
Qy	1887	ATACATGTGTAGTTTCCAAAGCACATAGCTAGAGAGAAATAATTTCTAGGAGCACTACC	1946	
Db	1446	ATACATGTGTAGTTTCCAAAGCACATAGCTAGAGAGAAATAATTTCTAGGAGCACTACC	1505	
Qy	1947	ATCTGTTTTCACATGAAATGCCACACACATAGAACTCCAAACACATCAATTTTCATTGCA	2006	
Db	1506	ATC-GTTTTCAACATGAAATGCCACACACATAGAACTCCAAACACATCAATTTTCATTGCA	1564	
Qy	2007	CAGACTGACTGTAGTTAAATTTTGTGCAGAACTCTATGAGACTGAATCTAAATGCTTCCAAA	2066	
Db	1565	CAGACTGACTGTAGTTAAATTTTGTGCAGAACTCTATGAGACTGAATCTAAATGCTTCCAAA	1624	
Qy	2067	ATGTTGTTTCTTGCAGAAATATCAAACTTGTATGCAAGAAATTTAAATTTACAAAATGA	2126	
Db	1625	ATGTTGTTTCTTGCAGAAATATCAAACTTGTATGCAAGAAATTTAAATTTACAAAATGA	1684	
Qy	2127	AGATTTATACCATTTGTGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCAATTTGTGAAC	2186	
Db	1685	AGATTTATACCATTTGTGTTTAAAGCTGTACTGAACTAAATCTGTGGAAGCAATTTGTAAAC	1744	
Qy	2187	TGTAAGAGCAAGATATCAATAAAGCTTATAGACTTAAATAAAAAAAGAAAAA 2240		
Db	1745	TGTAAGAGCAAGATATCAATAAAGCTTATAGACCCTTATAGACCCAAAGCAAAAAA 1798		
RESULT 12				
ABK34580				
ID	ABK34580 standard; cDNA; 1514 BP.			
XX	ABK34580;			
XX	08-MAY-2002 (first entry)			
XX	Human cDNA for novel secreted protein, SEQ ID 349.			
XX	Human; ss; gene; secreted protein; immune deficiency; viral infection;			
KW	bacterial infection; fungal infection; autoimmune disorder; burn;			
KW	rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;			
KW	diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;			
KW	Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;			
KW	coagulation disorder; haemophilia; inflammatory disorder; ulcer;			
KW	tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;			
XX	Lymphoid cell deficiency.			
OS	Homo sapiens.			
XX	WO200177290-A2.			
FN	18-OCT-2001.			
XX	29-MAR-2001; 2001WO-US010295.			
XX	06-APR-2000; 2000US-0194941P.			
PR	(GEM) GENETICS INST INC.			
XX	Wong CG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;			
PI	Gulukota K, Graham JR;			
XX	WPI; 2002-179323/23.			
XX	Six hundred and twenty five polynucleotides derived from a variety of			

human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders.

Claim 1; Page 173; 339pp; English.

The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell transformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopoiesis, for treating myeloid or lymphoid cell deficiencies. The present sequence is one of the 625 cDNA sequences encoding a secreted protein

Sequence 1514 BP; 455 A; 258 G; 313 G; 488 T; 0 U; 0 Other;

Query Match 65.8%; Score 1473.4; DB 6; Length 1514;
Best Local Similarity 99.1%; Pred. No. 2e-297;
Matches 1504; Conservative 0; Mismatches 6; Indels 7; Gaps 2;

QY	724	AGAAGACTGGAGTGGTGGTGGCCAGCCATTCTGCTGCTTCATTGACAGTATTCA	783
DB	1	AGAAGACTGGAGTGGTGGTGGCCAGCCATTCTGCTGCTTCATTGACAGTATTCA	60
QY	784	GCATTGTGAGGTACAGCTACATTGCTGGCCCTGCTCTGTGTGACCATCAGCTTTA	843
DB	61	GCATTGTGAGGTAAACGCTACATTGCTGGCCCTGCTCTGTGTGACCATCAGCTTTA	120
QY	844	GGATATACAAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCATTCAGGG	903
DB	121	GGATATACAAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCATTCAGGG	180
QY	904	CATATCTGGAATCTGAAGTGTGCTATATCTGAGGAGTGGTTCAGAAGTACAGTAATCTG	963
DB	181	CATATCTGGAATCTGAAGTGTGCTATATCTGAGGAGTGGTTCAGAAGTACAGTAATCTG	240
QY	964	CTCTTGGTTCATGTGAATGACGATAAAGGAACCTCAGCGCCTCTCTTAGTTGATGATT	1023
DB	241	CTCTTGGTTCATGTGAATGACGATAAAGGAACCTCAGCGCCTCTCTTAGTTGATGATT	300
QY	1024	TAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCTTGT	1083
DB	301	TAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCTTGT	360
QY	1084	TTAATGTCCTGACACTACTGATTTGGCTCTCATTTTCATCTTCTGAGTTCCTGTTATTT	1143
DB	361	TTAATGTCCTGACACTACTGATTTGGCTCTCATTTTCATCTTCTGAGTTCCTGTTATTT	420
QY	1144	ATGAACGGCATCAGGCACAGATAGATCAATTCATAGGACTTGCAGATGAAGATGTTAAG	1203
DB	421	ATGAACGGCATCAGGCACAGATAGATCAATTCATAGGACTTGCAGATGAAGATGTTAAG	480
QY	1204	ATGCTATGGTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGAAAC	1263
DB	481	ATGCTATGGTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGAAAC	540
QY	1264	GCCCAAAATATATAGTAGAGTTCATCTTTAAAGGGGATATTCATTGATATACGGGG	1323
DB	541	GCCCAAAATATATAGTAGAGTTCATCTTTAAAGGGGATATTCATTGATATACGGGG	600

QY	1324	AGGGTCAGGGAAGAACGAACCTTGACGTTGCGAGTGCAGTTCACAGATCGTTGTTAGATC	1383
DB	601	AGGGTCAGGGAAGAACGAACCTTGACGTTGCGAGTGCAGTTCACAGATCGTTGTTAGATC	660
QY	1384	TTTATTTTATAGCCATGCACTGTTGTGAGGAAAAATTAACCTGCTTGTGACATGTCATC	1443
DB	661	TTTATTTTATAGCCATGCACTGTTGTGAGGAAAAATTAACCTGCTTGTGACATGTCATC	720
QY	1444	ATCATCTTAAGTATTTGTAAGCTGCTATGTAAGGATTTAAACCGTAATCATATCTTTTC	1502
DB	721	ATCATCTTAAGTATTTGTAAGCTGCTATGTAAGGATTTAAACCGTAATCATATCTTTTC	780
QY	1503	---CTATCTGAGGCACTGGTGGAAATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGT	1559
DB	781	TATCTATCTGAGGCACTGGTGGAAATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGT	840
QY	1560	CTTGGCGCATCTTGGCAAGTTGCGAGAGATGTGGAGCTAGAAAAAAGGAGGAGGAGGAGG	1619
DB	841	CTTGGCGCATCTTGGCAAGTTGCGAGAGATGTGGAGCTAGAAAAAAGGAGGAGGAGGAGG	900
QY	1620	TTTTTCAGTTTGTGCACTGCTGATGCTCGCTGATGATTTGATGATGATGATGATGATGATG	1679
DB	901	TTTTTCAGTTTGTGCACTGCTGATGCTCGCTGATGATTTGATGATGATGATGATGATGATG	960
QY	1680	TGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGAGATGACAAAGCTTGTCTTCTGCTGA	1739
DB	961	TGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGAGATGACAAAGCTTGTCTTCTGCTGA	1020
QY	1740	TGTTTCTAGGCTATTTGTGACATTTTACCTGTTATATATTAATGTCATATATGATGATGATG	1799
DB	1021	TGTTTCTAGGCTATTTGTGACATTTTACCTGTTATATATTAATGTCATATATGATGATGATG	1080
QY	1800	TTATATATGATGATGTTTTCACAAAGCTTACAGCTTTCAGCTTCCAGCCACCCACAGTGC	1859
DB	1081	TTATATATGATGATGTTTTCACAAAGCTTACAGCTTTCAGCTTCCAGCCACCCACAGTGC	1140
QY	1860	TTGATATTTTCAGAGTCACTGATGTTTATATATGATGATGATGATGATGATGATGATGATG	1919
DB	1141	TTGATATTTTCAGAGTCACTGATGTTTATATATGATGATGATGATGATGATGATGATGATG	1200
QY	1920	AGAGAAATATTTTCAGAGCACTACCAATCTGTTTTCACAAATGAAATGCCACACATAG	1979
DB	1201	AGAGAAATATTTTCAGAGCACTACCAATCTGTTTTCACAAATGAAATGCCACACATAG	1260
QY	1980	AACTCCACACACATCAATTTTCATTTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2039
DB	1261	AACTC---CAACATCAATTTTCATTTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1317
QY	2040	TATGAGCTGAATCTAATGCTTCCAAATATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT	2099
DB	1318	TATGAGCTGAATCTAATGCTTCCAAATATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT	1377
QY	2100	TGCAAGAAATTTAATTTACAAATGAAGATTTATACATTTGGTGTGTTGTTGTTGTTGTTGTT	2159
DB	1378	TGCAAGAAATTTAATTTAATGAAGATTTATACATTTGGTGTGTTGTTGTTGTTGTTGTTGTT	1437
QY	2160	ACTAAATCTGGAATGCAATGCTGTAAGGAAAGTATCAATTAAGCTTATAGAC	2219
DB	1438	ACTAAATCTGGAATGCAATGCTGTAAGGAAAGTATCAATTAAGCTTATAGAC	1497
QY	2220	TTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2236
DB	1498	GTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1514

RESULT 13
AAD08386
ID AAD08386 standard; cDNA; 1683 BP.
XX AAD08386;
XX 09-AUG-2001 (first entry)


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QY 901 GGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTGAGAGTACAGTAATT 960
Db 996 GGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTGAGAGTACAGTAATT 1055
QY 961 CTGCTCTTGGTCATGTAAGTACGACGATAAAGGAATCAGGGCCCTCTTCTAGTTGATG 1020
Db 1056 CTGCTCTTGGTCATGTAAGTACGACGATAAAGGAATCAGGGCCCTCTTCTAGTTGATG 1115
QY 1021 ATTAGTTGATTTCTGTAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCT 1080
Db 1116 ATTAGTTGATTTCTGTA----- 1134
QY 1081 TGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCTCAGTGTCTGTGA 1140
Db 1135 -----GCTCTCAATTTCACTCTTCTCAGTGTCTGTGA 1165
QY 1141 TTTATGAAGCGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCATAAATGAATGTTA 1200
Db 1166 TTTATGAAGCGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCATAAATGAATGTTA 1225
QY 1201 AAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAAAGCTGAATGAA 1260
Db 1226 AAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAAAGCTGAATGAA 1285
QY 1261 AACGCCCAAAATAATTAGTAGGAGTTTCATCTTTAAAGGGGATATTTCAITTTGATTATACGG 1320
Db 1286 AACGCCCAAAATAATTAGTAGGAGTTTCATCTTTAAAGGGGATATTTCAITTTGATTATACGG 1345
QY 1321 GGGAGGGTCAGGAAGAAGAACCTTGAGCTTGAGTGCAGTGTTCACAGATCGTTGTTAG 1380
Db 1346 GGGAGGGTCAGGAAGAAGAACCTTGAGCTTGAGTGCAGTGTTCACAGATCGTTGTTAG 1405
QY 1381 ATCTTTATTTTTPAGCATGCTGTTGTGAGGAAAAATTAACCTGCTTGTGACTGCCATGTG 1440
Db 1406 ATCTTTATTTTTPAGCATGCTGTTGTGAGGAAAAATTAACCTGCTTGTGACTGCCATGTG 1465
QY 1441 TTCAATCATCTTAAGTATTGTAAAGCTGCTATGATGGATTTAAACCGTAATCATATCTTTT 1500
Db 1466 TTCAATCATCTTAAGTATTGTAAAGCTGCTATGATGGATTTAAACCGTAATCATATCTTTT 1525
QY 1501 TCCTATCTGAGGCATCTGGTGNATAAAAAACCTGTATATTTTACTTTGTCAGATAGTC 1560
Db 1526 TCCTATCTGAGGCATCTGGTGNATAAAAAACCTGTATATTTTACTTTGTCAGATAGTC 1585
QY 1561 TTGCGGCATCTTGGCAAGTTGCGAGAGATGTTGGAGCTAGAAAAAAGAAAAA 1615
Db 1586 TTGCGGCATCTTGGCAAGTTGCGAGAGATGTTGGAGCTAGAAAAAAGAAAAA 1640
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RESULT 14

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ABV94680
ID ABV94680 standard; cDNA; 4632 BP.
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AC ABV94680;
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DT 14-JAN-2003 (first entry)
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DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.
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XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
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OS Homo sapiens.
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XX WO200260317-A2.
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PN 08-AUG-2002.
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PF 30-JAN-2002; 2002WO-US002781.
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XX 30-JAN-2001; 2001US-0265305P.
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PR 31-JAN-2001; 2001US-0265682P.
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PR 09-FEB-2001; 2001US-0267568P.
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PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0333999P.
PR 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI WPI; 2002-627435/67.
XX P-PSDB; ABP68600.
DR New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;
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Query Match 62.9%; Score 1409; DB 6; Length 4632;

Best Local Similarity 96.1%; Pred. No. 8.2e-284;

Matches 1479; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

QY 693 GTTGTTCACCTCCCTGTAAGAGAGACATTAAGAGAGCTGGAGTGGTCTTTGGTGCCAGC 752

Db 3154 GTTGTTCACCTCCCTGTAAGAGAGACATTAAGAGAGCTGGAGTGGTCTTTGGTGCCAGC 3213

QY 753 CTATTTCCTGCTGCTTTCATTGACAGATTTACAGCTTTGTGACGCTAACAGCCTACATTGCC 812

Db 3214 CTATTTCCTGCTGCTTTCATTGACAGATTTACAGCTTTGTGACGCTAACAGCCTACATTGCC 3273

QY 813 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCAAGCTATC 872

Db 3274 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCAAGCTATC 3333

QY 873 CAGAAATCAGATGAAGCCACCATTTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 932

Db 3334 CAGAAATCAGATGAAGCCACCATTTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 3393

QY 933 GAGGAGTTGGTTCAGAGATCAGTAATTTCTGCTCTTGGTTCATGTGAATCTGCACGCAATAAG 992

Db 3394 GAGGAGTTGGTTCAGAGATCAGTAATTTCTGCTCTTGGTTCATGTGAATCTGCACGCAATAAG 3453

QY 993 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTTCTTGAAGTTTGCAGTGTG 1052

Db 3454 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTTCTTGAAGTTTGCAGTGTG 3513

QY 1053 ATGTGGGTATTACCTATGTTGGTCCCTTGTGTTAATGTCTGACACTACTGATTTTGGCT 1112

Db 3514 ATGTGGGTATTACCTATGTTGGTCCCTTGTGTTAATGTCTGACACTACTGATTTTGGCT 3573

QY 1113 CTCATTTCACTCTTTCAGTGTTCCTGTTTATTTATGAAGCGCATCAGGCAAGATAGATCAT 1172

Db	3574		CTCATTTTCACTTCTTCAGTGTTCCTGTTATTTATGAAACGGCATCAGGCACAGATAGATCAT	3633
Qy	1173	TATCTAGGACTTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAATATCCAAAGCAAAAATC	1232	
Db	3634	TATCTAGGACTTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAATATCCAAAGCAAAAATC	3693	
Qy	1233	CCTGGATTGAAGCGCAAGCTGGAATGAAGCCCAAAATTAATTAGTAGGAGTTTCATCTTT	1292	
Db	3694	CCTGGATTGAAGCGCAAGCTGGAATGAAGCCCAAAATTAATTAGTAGGAGTTTCATCTTT	3753	
Qy	1293	TAAAGGGGATATTCATTTGATTATACGGGGGAGGTCAGGGAAGAACGAACTTGACGTT	1352	
Db	3754	TAAAGGGGATATTCATTTGATTATACG-----GATCTTATTTTAGCCATGCTTTGATAGATCTTTATTTT	3780	
Qy	1353	GCAGTCGAGTTTTCACAGATCGTTGTATAGATCTTTATTTTTAGCCATGCATGTTGTGAGG	1412	
Db	3781	-----GATCTTATTTTAGCCATGCTTTGATAGATCTTTATTTTTAGCCATGCATGTTGTGAGG	3813	
Qy	1413	AAAAATTACCTGCTTGACTGCCAATGTTTCATCATCTTAAGTATGTAAAGCTGCTATGT	1472	
Db	3814	AAAAATTACCTGCTTGACTGCCAATGTTTCATCATCTTAAGTATGTAAAGCTGCTATGT	3873	
Qy	1473	ATGATTTTAAACCGTATCATATCTTTTCTATCTGAGGCACCTGGTGGATATAAAACC	1532	
Db	3874	ATGATTTTAAACCGTATCATATCTTTTCTATCTGAGGCACCTGGTGGATATAAAACC	3933	
Qy	1533	TGTATATTTTACTTGTGTGCAGATAGTCTTGCAGCATCTTGGCAAGTTGCAGAGATGGTG	1592	
Db	3934	TGTATATTTTACTTGTGTGCAGATAGTCTTGCAGCATCTTGGCAAGTTGCAGAGATGGTG	3993	
Qy	1593	GAGCTAGAAAAAATAAAAGCCCTTTTCAGTTTGTGCATCTGTGTATGGTCCGTTGA	1652	
Db	3994	GAGCTAGAAAAAATAAAAGCCCTTTTCAGTTTGTGCATCTGTGTATGGTCCGTTGA	4053	
Qy	1653	GATTTATGTCAGATTTTCTGAAATCGAATGTTTGTATTAGACGAGATCATACCGGTAAGACA	1712	
Db	4054	GATTTATGTCAGATTTTCTGAAATCGAATGTTTGTATTAGACGAGATCATACCGGTAAGACA	4113	
Qy	1713	GGAATGACAAAGCTTGCTTTTCTGATGTTCTAGGTGTTATGTTGACCTTTTACTGTTTATA	1772	
Db	4114	GGAATGACAAAGCTTGCTTTTCTGATGTTCTAGGTGTTATGTTGACCTTTTACTGTTTATA	4173	
Qy	1773	TTAATTGCCAATATAAGTAAATATAGATTTATATATATGTTGTTTTCACAAAGCTTAGAC	1832	
Db	4174	TTAATTGCCAATATAAGTAAATATAAGATTTATATATGTTGTTTTCACAAAGCTTAGAC	4233	
Qy	1833	CTTTTACCTTCCAGGCCACCCACAGTCTGTGATTTTCAGAGTCAGTCAATTTGGTTATACAT	1892	
Db	4234	CTTTTACCTTCCAGGCCACCCACAGTCTGTGATTTTCAGAGTCAGTCAATTTGGTTATACAT	4293	
Qy	1893	GTGTAGTTTCCAAAGCACATAGCTAGAGAAGAAATATTTCTAGAGCAGCTACCATCTGT	1952	
Db	4294	GTGTAGTTTCCAAAGCACATAGCTAGAGAAGAAATATTTCTAGAGCAGCTACCATCTGT	4353	
Qy	1953	TTTCAACATGAAATGCCACACACATAGAACTTCCAAACATCAATTTCAITGACAGACT	2012	
Db	4354	TTTCAACATGAAATGCCACACACATAGAACTTCCAAACATCAATTTCAITGACAGACT	4413	
Qy	2013	GACTGTAGTTAAATTTTGTTCAGAAATCTATGGAATCTAATGCTTCCAAAAATGTTG	2072	
Db	4414	GACTGTAGTTAAATTTTGTTCAGAAATCTATGGAATCTAATGCTTCCAAAAATGTTG	4473	
Qy	2073	TTTGTGTTGCAAAATCAAACTTGTATGCAAGAAATTTAATTAACAAATGAAATTT	2132	
Db	4474	TTTGTGTTGCAAAATCAAACTTGTATGCAAGAAATTTAATTAACAAATGAAATTT	4533	
Qy	2133	ATACCATTTGTGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCATTTGTGAACGTAAA	2192	
Db	4534	ATACCATTTGTGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCATTTGTGAACGTAAA	4593	
Qy	2193	AGCAAGTATCAATAAAGCTTTATAGACTTAAAAAATAA 2231		

4594 AGCAAAGTATCAATAAAGCTTATAGACTTAAAAA 4632

RESULT 15
ADG32772
ID ADG32772 standard; DNA; 4632 BP.
XX
AC ADG32772;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human DNA differentially expressed in patients with SLE SeqID96.
XX
KW human; ds; autoimmune; chronic inflammatory disease; SLE;
KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW diverticulitis; primary biliary sclerosis.
XX
OS Homo sapiens.
XX
FN WO2003090694-A2.
XX
PD 06-NOV-2003.
XX
PF 24-APR-2003; 2003WO-US013015.
XX
PR 24-APR-2002; 2002US-00131827.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgenuth J, Fry K, Woodward R, Ly N;
XX
DR WPI; 2003-877243/81.
XX
PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT colitis, psoriasis and asthma by detecting the expression level of one or
PT more genes.
XX
PS Claim 18; SEQ ID NO 96; 877pp; English.
XX
CC This invention relates to novel methods for diagnosing and monitoring
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC the identification of genes that have a clinical utility as diagnostic
CC tools for the management of, in particular, patients with systemic lupus
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC present invention describes a method for determining the levels of
CC multiple differentially expressed genes of a patient, in a concerted
CC manner, in order to achieve an improved diagnostic assay with sensitivity
CC and specificity for the disease in question. As such, these genes are
CC useful for the diagnosis of various other inflammatory disorders
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC This polynucleotide is a DNA sequence representing human mRNA that is
CC differentially expressed in patients with SLE, used in an exemplification
CC of the invention.
XX
SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;
Query Match 62.9%; Score 1409; DB 10; Length 4632;
Best Local Similarity 96.1%; Pred. No. 8.2e-284;
Matches 1479; Conservative 0; Mismatches 0; Indels 60; Gaps 1

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QY 753 CTATTCTGCTGCTTCAATTCACAGTATTCAGCATTCGTGCGGTAAACGCTACATTGCC 812
Db 3214 CTAATCTGCTGCTTCAATTCACAGTATTCAGCATTCGTGCGGTAAACGCTACATTGCC 3277

QY	813	TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAAGCTATC	872
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QY	873	CAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAACTCTGAAGTTGCTATATCT	932
Db	3334	CAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAACTCTGAAGTTGCTATATCT	3393
QY	933	GAGGAGTTGGTTCAGAACTCAGATAATCTCTGCTCTTGGTCTATGTGAACTGCACGATAAAG	992
Db	3394	GAGGAGTTGGTTCAGAACTCAGATAATCTCTGCTCTTGGTCTATGTGAACTGCACGATAAAG	3453
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QY	1053	ATGTGGGTATTTTACCTATGTTGGTGCCCTGTTTAAATGCTGACACTACTGATTTTGGCT	1112
Db	3514	ATGTGGGTATTTTACCTATGTTGGTGCCCTGTTTAAATGCTGACACTACTGATTTTGGCT	3573
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Db	3574	CTCATTTTCACTCTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCAACAGATGATCAT	3633
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Db	3874	ATGGATTTAAACCGTAATCATATCTTTTTCCTATCTGAGGCACTGGTGGAAATAAAAAACC	3933
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QY	1713	GGAATGACAAAGCTTTTCTGATGTTTCTAGGTGTAATTTGACITTTTACTGTTATA	1772
Db	4114	GGAATGACAAAGCTTTTCTGATGTTTCTAGGTGTAATTTGACITTTTACTGTTATA	4173
QY	1773	TTAATTGCCAATATTAAGTAATAATATAGATATATATAGTATAGTTTTCAAAGCTTAGAC	1832
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Job time : 1124 secs

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Db	4474	TTTGTGTCAAATATCAACATTTGTTATGCAAGAAATTTATTAATTACAAATGAAGATTT	4533
QY	2133	ATACCATTTGTGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCAATTTGTAACCTGTA	2192
Db	4534	ATACCATTTGTGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCAATTTGTAACCTGTA	4593
QY	2193	AGCAAGTATCAATAAAGCTTTATAGACTTAAAAAATAA 2231	
Db	4594	AGCAAGTATCAATAAAGCTTTATAGACTTAAAAAATAA 4632	

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2005, 13:22:45 ; Search time 6519 Seconds
(without alignments)
13079.301 Million cell updates/sec

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Perfect score: 2240
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 69479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_htc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gesi.*
9: gb_gesi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1488.8	66.5	1798	3 AF125103	AF125103 Homo sapi
2	1359.2	60.7	1785	3 AF077050	AF077050 Homo sapi
3	1355	60.5	1540	3 CR611869	CR611869 full-leng
4	1035.4	46.2	3533	3 AK034902	AK034902 Mus muscu
5	957.4	42.7	1097	5 BX439214	BX439214 BX439214
c	6	917.2	40.9	1028	5 BX426504 BX426504
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	8	881.2	39.3	911	1 AL549191 AL549191
c	9	861.2	38.4	875	1 AL573494 AL573494
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	12	837.2	37.4	901	5 BQ879359
	13	831.8	37.1	1164	7 CK232009
	14	831	37.1	956	7 CN644030
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	16	815.6	36.4	987	7 CO647477
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	19	797.6	35.6	910	5 BQ959498
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	21	779.8	34.8	1002	5 BX462171
	22	779.6	34.8	1022	4 BM557554
	23	776.2	34.7	983	7 CN803408
c	24	775	34.6	787	5 BQ774392

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26	771.8	34.5	1008	7	CN801982	CN801982	ILLUMIGEN
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28	771.4	34.4	920	7	CN644247	CN644247	ILLUMIGEN
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ALIGNMENTS

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LOCUS Homo sapiens neuroendocrine specific protein c homolog mRNA,
DEFINITION complete cds.
ACCESSION AF125103
VERSION AF125103.1 GI:5107001
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1798)
AUTHORS Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W.,
Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z.
Cloning and functional analysis of cDNAs with open reading frames
for 300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells
JOURNAL Genome Res. 10 (10), 1546-1560 (2000)
MEDLINE 20499367
PUBMED 11042152
REFERENCE 2 (bases 1 to 1798)
AUTHORS Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H.,
Dai, M., Huang, Q., Chen, S. and Chen, Z.
Human neuroendocrine specific protein c homolog mRNA, complete cds
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1798)
AUTHORS Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H.,
Dai, M., Huang, Q., Chen, S. and Chen, Z.
Direct Submission
TITLE Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai
JOURNAL Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P. R. China
FEATURES
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1. 1798
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ORIGIN

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Best Local Similarity 99.1%; Pred. No. 0;
Matches 1540; Conservative 0; Mismatches 7; Indels 7;

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RESULT 2
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complete cds.
ACCESSION AF077050.1 GI:4689147
VERSION AF077050
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1785)
AUTHORS Song,H., Peng,Y., Zhou,J., Huang,Q., Dai,M., Mao,Y., Yu,Y., Xu,X.,
Luo,B., Hu,R. and Chen,J.
TITLE Human neuroendocrine-specific protein C (NSP) homolog gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1785)
AUTHORS Song,H.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute of
Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II,
Shanghai 200025, P.R. China
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ORIGIN
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Best Local Similarity 99.1%; Pred. No. 1.7e-288;
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Db 1086 CTGTATATTTTACCTTTGTCAGATAGTCTTTGCCGCACTTTGGCAAGTTGCAGATGGT 1145
Qy 1592 GGAGCTAG-AAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1650
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Db 1146 GGAGCTAGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1205
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Qy 1711 CAGGAATGACAAAGCTTGTCTTCTGATGTTCTAGGTGATTTGTGACCTTTTACTCTGTA 1770
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Qy 1771 TATTAAATGCAATATAAGTAAATATAGATTATATATATATATATATATATATATATATAT 1830
Db 1326 TATTAAATGCAATATAAGTAAATATAGATTATATATATATATATATATATATATATATAT 1385
Qy 1831 ACCTTTACCTTCCAGCCACCCACAGCTGCTTGTATATTTTGTAGAGTCACTCATTTGGTTATAC 1890
Db 1386 ACCTTTACCTTCCAGCCACCCACAGCTGCTTGTATATTTTGTAGAGTCACTCATTTGGTTATAC 1445
Qy 1891 ATGTGTAGTTTCCAAAGCACATNAAGCTAGAGAGAGAAATATTTCTAGGAGCACTACCATCT 1950
Db 1446 ATGTGTAGTTTCCAAAGCACATNAAGCTAGAGAGAGAAATATTTCTAGGAGCACTACCATCT 1505
Qy 1951 GTTTTCAACATGAAATGCCACACACATAGAACTCCAAACACATCAATTTTCAATTCACAGA 2010
Db 1506 GTTTTCAACATGAAATGCCACACACATAGAACTCCAAACACATCAATTTTCAATTCACAGA 1565
Qy 2011 CTGACTGTAGTTAAATTTGTGACAGAACTATGAGACTGAATCTTAATGCTTCCAAAATGT 2070
Db 1566 CTGACTGTAGTTAAATTTGTGACAGAACTATGAG-CTGAATCTTAATGC-TCCAAAATGT 1623
Qy 2071 TGTTTGTTCCAATATCAACATTTGTTATGCAAGAAATAT 2112
Db 1624 TGTTTGT--GCAATACCAACATTTGTTATGCAAGAAATTTT 1663

RESULT 3
CR611869 LOCUS 1540 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DN004YJ08 of Adult brain of Homo sapiens
(human).
ACCESSION CR611869
VERSION 1 GI:50492676
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1540)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1540)
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .1540
organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
clone="CS0DN004YJ08"
tissue_type="Adult brain"
plasmid="pCMVSPORT_6"
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ORIGIN

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Query Match          60.5%; Score 1355; DB 3; Length 1540;
Best Local Similarity 99.5%; Pred. No. 1.4e-287;
Matches 1382; Conservative 0; Mismatches 0; Indels 7; Gaps 2;

QY 692 GGTGTTGACCTCCTGTTACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAG 751
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QY 752 CCTATTCTGCTGCTTCATTTGACACAGTATTCAGCATTCTGAGCGTAAACAGCCTACATTC 811
Db 215 CCTATTCTGCTGCTTCATTTGACACAGTATTCAGCATTCTGAGCGTAAACAGCCTACATTC 274

QY 812 CTGTGCCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGTGTGATCCAAAGCTAT 871
Db 275 CTGTGCCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGTGTGATCCAAAGCTAT 334

QY 872 CCAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGAAAGTTGCTATATC 931
Db 335 CCAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGAAAGTTGCTATATC 394

QY 932 TGAGAGTGGTTCAGAGTACAGTAATCTGCTCTTGGTCACTGTGAACCTGCACAGTAAA 991
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QY 992 GGAACCTCAGGGCCCTCTCTTAGTTGATGATTAGTTGATTTCTGTAATCTCTGAAGTTTGCAAGTGT 1051
Db 455 GGAACCTCAGGGCCCTCTCTTAGTTGATGATTAGTTGATTTCTGTAATCTCTGAAGTTTGCAAGTGT 514

QY 1052 GATGTGGGTATTTACTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTTGGC 1111
Db 515 GATGTGGGTATTTACTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTTGGC 574

QY 1112 TCTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGTCA 1171
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QY 1472 TATGGAATTAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACCTGGTGGATAAA 1527
Db 935 TATGGAATTAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACCTGGTGGATAAA 994

QY 1528 AAACCTGATATTTTACTTTGTTGAGATAGTCTTGGCGCATCTTGGCAAGTTGCAGAGA 1587
Db 995 AAACCTGATATTTTACTTTGTTGAGATAGTCTTGGCGCATCTTGGCAAGTTGCAGAGA 1054

QY 1588 TGGTGGAGCTAGAAAAAAGAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCC 1647
Db 1055 TGGTGGAGCTAGAAAAAAGAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCC 1114

QY 1648 GTGTAGATTGATGAGATTTTCTGAAATGAAATGTTTGTGTAGACGAGATCATACCGGTA 1707
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QY 1708 AAGCAGGAATGACAAAGCTTGTCTTTCTGGTATGTTCTAGGTGATTTGTGACTTTTACTG 1767
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Db 1295 TAGACCTTTTACCTTCCAGCCACCCACAGCTGCTTGTATATTTTCAGAGTCAGTCATTGGTTA 1354

QY 1888 TACATGTGTAGTTTCCAAAGCACAATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCA 1947
Db 1355 TACATGTGTAGTTTCCAAAGCACAATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCA 1414

QY 1948 TCTGTTTTCACATGAATGCCACACACATAGAACTCCAAACATCAATTTTCATTGTCAC 2007
Db 1415 TCTGTTTTCACATGAATGCCACACACATAGAACTCCAAACATCAATTTTCATTGTCAC 1471

QY 2008 AGACTGACTGTAGTTAAATTTTGTTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAAA 2067
Db 1472 AGACTGACTGTAGTTAAATTTTGTTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAAA 1531

QY 2068 TGTGTTTGTG 2076
Db 1532 TGTGTTTGTG 1540

RESULT 4
AK034902
LOCUS
DEFINITION
Mus musculus 12 days embryo mRNA linear HTC 03-APR-2004
and neck cDNA, RIKEN full-length enriched library, clone:9430089L06
product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO PROTEIN)
(FOOCN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus
norvegicus], full insert sequence.
ACCESSION
AK034902
VERSION
AK034902.1 GI:26084268
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20499374
11042159
4
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
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JOURNAL
MEDLINE
PUBMED
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TITLE
JOURNAL
MEDLINE
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REFERENCE
```

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE Nature 409, 685-690 (2001)

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE Nature 420, 563-573 (2002)

AUTHORS 6 (bases 1 to 3533)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saigo, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@ac.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: <http://genome.gsc.riken.jp/> URL: <http://fantom.gsc.riken.jp/>

FEATURES Location/Qualifiers

1..3533

`/organism="Mus musculus"`

`/mol_type="mRNA"`

`/strain="C57BL/6J"`

`/db_xref="FANTOM DB:9430059L06"`

`/db_xref="taxon:10090"`

`/clone="9430059L06"`

`/tissue_type="embryonic body between diaphragm region and neck"`

`/clone_lib="RIKEN full-length enriched mouse cDNA library"`

`/dev_stage="12 days embryo"`

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`/note="RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOCO PROTEIN) (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog (Rattus norvegicus) (SWISSPROT|Q9UK11, evidence: FASTA, 95.8%ID, 100%length, match=1068)"`

misc_feature

1..3533

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ORIGIN

Query Match 46.2%; Score 1035.4; DB 3; Length 3533;

Best Local Similarity 77.0%; Pred. No. 4.5e-217;

Matches 1710; Conservative 0; Mismatches 341; Indels 170; Gaps 30;

Qy 19 CTCGGCTCAGTCGGCCAGCCCTCTCAGTCTCCCAACCCCAACCGCCGCGGCT 78

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Db 186 CTGAG--GAGAAGTGGCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 236

Qy 139 TGGAGACCTGGACGAGTCTCTCTGGT---CTGCTCTGGACAGCGCCACCGCGCG 195

Db 237 TGGAGACATAGACGAGTCGTCTGGTCTCTCTGTCGGCGGATAGCCCGCGCGCC 296

196 AGCCCGGTTCAAGTACCAGTTCGTGAGGAGCCCGGAGGACGAGGAGAGAGAGAGG 255

Db 297 CGCCCGCTTTCAAGTACCAGTTCGTGAGGAGCCCGGAGGACGAGGAGAGAGAGAG 356

Qy 256 AGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 315

Db 357 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 416

Qy 316 CCGCCCGGGCTGTCCCGGGGCCCGGAGTCCACCGCCCTGCGCGCGCGCGCCCTGATGG 375

Db 417 CAGCGCGGGCTGTCCCGGGGCTCCGGTCCGCTGCGGCTGCGGCTGCTGCGG 467

Qy 376 ACTTCGGAATGATCTGTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 435

Db 468 ACTTCAGCAGCAGTCTGGTGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 527

Qy 436 TCGCCCGGAGCGGAGCGGCTCTTTGGACCCCGGAGCCCGGCTGCTGCGACCGTGC 495

Db 528 CCGCCCTTGAGAGGCGGCGGCTCTGCGAACGAGCGCCCGCGGCGT-----CCGCGC 578

Qy 496 CATCCCGCTGTCTGCTGCGCGAGTCTCGCCCTCCCAAGCTCCCTGAGGAGGAGCGAGCCTC 555

Db 579 CATCCCTGCGCGCGCTGCGCGAGTCTGCGCTCCCAAGCTCCCGGAGGAGCGAGCCTG 638

Qy 556 CGCGCGCGCTCCCGCTCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 615

Db 639 CAGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 670

Qy 616 CCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 675

Db 671 -----CCCCCTATTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 725

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Qy 736 TGTGTTTGGTGCAGCTTATCTGCTGCTTTCAATGACAGTATTGAGCAATTTGAGCG 795

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Qy 796 TACAGCTCATTTGCTGGCGCTGCTCTCTGACCATCAGCTTTAGGATATACAGG 855

Db 843 TAAACGGCTCATTTGCTGGCGCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGG 902

Qy 856 GTGTGATCCAAAGCTATCCAGAAATCAGATGAAGCGCACCCATTCAGGCGCATATCTGCAAT 915

Db 903 GTGTGATCCAAAGCTATCCAGAAATCAGATGAAGCGCACCCATTCAGGCGCATATTTGCAAT 962

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Db 1143 CACTACTGATTTTGGCTCTCATTTCACTCTTCAGTATTTCTGTTATATATGAACGGCATC 1202

Qy 1156 AGGACAGATAGATCATTTATCTAGGACTTGCATTAAGAATGTTAAAGATGCTATGGCTA 1215

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Db 1263 AATCCAAAGCAAAATCCCTGGGATGAAGCGCAAGCTGAATGAAAGGCCCAAA----- 1318


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QY 1336 GAACGAACCTTGACCTTGCAGTGCAGTTCACAGATCGTTGTAGATCTTTATTTTACG 1395
Db 1375 GGGGTGAGCCCTGGGTGGCGCGTGCAGTTCA-----GTTATTTTATGAC 1417
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QY 1685 GTTTAGACAGATCATACCGGTAAAGCAGGAATGACAAAGCTGTGTTTCTGTTATGTTTC 1744
Db 1713 -----AGATGAGCATACTACTAAAGCA--GAGTGGAAAAATCTGTCTTTTATGGTATGTT 1765
QY 1745 TAGGTGTTATGTTGACTTTTACTGTTTATTAATTCGCAATATAAGTAATAATAG--ATTA 1802
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QY 1862 GATATTTGAGTGCAGTCACTTGGTTTATACATGTGTAGTTCGCAAGCACAATAGCTAGAAG 1921
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QY 1922 AAGAAATATTTCTAGGAGCACTTACCATCTGTTTTCACATGAATGAATGCCACACACATAGAA 1981
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QY 1982 CTCCAACAACATCAATTTTCATTGCAAGACTGTAGTTAAATTTTGTACAGAAATCTA 2041
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QY 2102 CAAGAAATTTAATTAACAATGAAGATTTATACCATTTGTTGTTTAAAGCTGTACTGAAC 2161
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Db 2193 A 2193
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RESULT 5
BX439214
LOCUS
DEFINITION BX439214 Homo sapiens PLACENTA 1097 bp mRNA linear EST 04-MAY-2004

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5-PRIME, mRNA sequence.  
BX439214  
BX439214.2 GI:47020895  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
Li W.B., Gruber C., Jessee, J. and Polayes, D.  
1 (bases 1 to 1097)  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 15, 2003 this sequence version replaced gi:30787776.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 1423.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DE008BD02QPl&c=1423.r.  
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."  
ORIGIN  
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Matches 959; Conservative 41; Mismatches 23; Indels 1; Gaps 1;  
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Db 75 CGTCACACACAGTACGTCCCTCGGCTCAGTCGGCCGACGCCCTCTCAGTCCTCCCAACCC 134  
QY 61 CCACACCGCCCGCGGCTCTTGAGACGCGGCCCGCCGCGCGCGCGCAGCAGCTGCAGCATC 120  
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QY 121 ATCTCCACCTTCAGACCATGGAAGACCTGGACCAAGTCTCTCTGCTCTGCTCTCGGACA 180  
Db 195 ATCTCCACCTTCAGACCATGGAAGACCTGGACCAAGTCTCTCTGCTCTGCTCTCGGACA 254  
QY 181 GCCCACCCCGCCCGCAGCCCGCTTCAAGTACCAAGTCTGTCAGGAGGAGCCGAGGACGAGG 240  
Db 255 GCCCACCCCGCCCGCAGCCCGCTTCAAGTACCAAGTCTGTCAGGAGGAGCCGAGGACGAGG 314  
QY 241 AGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
Db 315 AGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374  
QY 301 TGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
Db 375 TGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 434  
QY 361 GCGCGCCCTTCATGACCTTCGGAATGACTTTCGTCGCGCGCGCCCGCGCGCGCCCGCGCG 420  
Db 435 GCGCGCCCTTCATGACCTTCGGAATGACTTTCGTCGCGCGCGCGCCCGCGCGCGCCCGCG 494  
QY 421 CGGCCGCTCCCGCGCTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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Db 495 CGGCGCTCCCGCTGCGCCGAGGCGGCGGCTCTTGGAGCCCGAGCCGGTGCTG 554
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Qy 541 AGGACGAGCGCTCCCGCGCCGCTCCCTCTCTCCCGCGGCGAGCGTGGAGCCCGCAGG 600
Db 615 AGGACGAGCGCTCCCGCGCCGCTCCCTCTCTCTCCCGCGGCGAGCGTGGAGCCCGCAGG 674
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Db 735 GGCCCAAGCGCAGGCGGCTCCCTCGGCGCTCAGTGTGTGTGACCTCTCTGTCTGGAGAGACA 794
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Qy 781 TCACCATTTGAGCGTAACGCTACATTCGCTGTGCGGCGGCTCTCTGTGTGACCATCAGCT 840
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Qy 841 TTAGGATATACAAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCGCCACCATCA 900
Db 915 TTAGGATATACAAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCGCCACCATCA 974
Qy 901 GGGCATATCTGAATCTGAAGTGTCTATATCTGAGGAGTGGTTCAGAAATCAGATGAAT 960
Db 975 GGGCATATCTGAATCTGAAGTGTCTATATCTGAGGAGTGGTTCAGAAATCAGATGAAT 1034
Qy 961 CTGCTCTGTGTCATGACCTGACGATGAAGGAGTCTCAGGCGCTCTCTTAGTTCATG 1020
Db 1035 YTRCTCTTGTGTCATGACCTGACGATGAAGGAGTCTCAGGCGCTCTCTTAGTTCATG 1093
Qy 1021 ATTT 1024
Db 1094 WTTT 1097

RESULT 6
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LOCUS
DEFINITION BX426504 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA
clone CS0DH001YJ01 3-PRIME, mRNA sequence.
ACCESSION BX426504
VERSION BX426504.2 GI:47012045
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1028)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30784554.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1423.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0AH001CE01NP1&c=1423.r.
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/clone="CS0DH001YJ01"
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/notes="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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ORIGIN

Query Match 40.9%; Score 917.2; DB 5; Length 1028;
Best Local Similarity 97.3%; Pred. No. 4e-191;
Matches 987; Conservative 2; Mismatches 10; Indels 15; Gaps 5;

Qy 1199 TAAAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATG 1258
Db 1011 TAAAGATGCTATGGCT- AAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATG 953
Qy 1259 AAAACGCGCCAAATTAATAGTAGAGTTTCATCTTTAAAGGGGATATTCATTTGATTATAC 1318
Db 952 AAAACGCGCCAAATTAATAGTAGAGTTTCATCTTTAAAGGGGATATTCATTTGATTATAC 893
Qy 1319 GGGGGAGGGTCCAGGAAGCAACCTTGACGTTGCAAGTGCAGTTTCACAGATCGTTGTT 1378
Db 892 GGGGGAGGGTCCAGGAAGCAACCTTGACGTTGCAAGTGCAGTTTCACAGATCGTTGTT 834
Qy 1379 AGATCTTTATTTTATGCGCATGCACTGTTGTGAGGAAAAATTAACCTGTTGACTGCCATG 1438
Db 833 AGATCTTTATTTTATGCGCATGCACTGTTGTGAGGAAAAATTAACCTGTTGACTGCCATG 774
Qy 1439 TGTTCATCATCTTAAGTATTTGTAAGTCTGATGTATGGATTAAACCGTAAATCATATCTT 1498
Db 773 TGTTCATCATCTTTAAGTATTTGTAAGTCTGATGTATGGATTAAACCGTAAATCATATCTT 714
Qy 1499 TTTC- ---CTATCTGAGGCACTGCTGGAATAAAAAACCTGTATATTTTACTTTGTTGTCAG 1554
Db 713 TTTCCTATCTATCTGAGGCACTGCTGGAATAAAAAACCTGTATATTTTACTTTGTTGTCAG 654
Qy 1555 ATAGTCTTTCGCGCATCTTGGCAAGTTGCAGAGATGTTGGAGCTAGAAAAA 1614
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Qy 1615 AGCCCTTTTCAGTGTGTGCACTGTGTATGTCGCTGTAGATTGATGAGATTTTCTGAAA 1674
Db 599 AGCCCTTTTCAGTGTGTGCACTGTGTATGTCGCTGTAGATTGATGAGATTTTCTGAAA 540
Qy 1675 TGAATCTTTGTTTATGACGAGATCATACCGTAAAGCAGCAATGACAAAGCTGCTTTTC 1734
Db 539 TGAATCTTTGTTTATGACGAGATCATACCGTAAAGCAGCAATGACAAAGCTGCTTTTC 480
Qy 1735 TGTGTATGTTCTAGTGTATTTGACCTTTTACTGTTATATTAATTTGCAATATAGTAAT 1794
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Qy 1855 AGTGTCTGATTTTTCAGAGTCAGTTCATGTTGTTATACATGTGTATGTTTCCAAAGCACA 1914
Db 359 AGTGTCTGATTTTTCAGAGTCAGTTCATGTTGTTATACATGTGTATGTTTCCAAAGCACA 300
Qy 1915 CTAGAAGAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAAACATGAATGCAACA 1974
Db 299 CTAGAAGAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAAACATGAATGCAACA 240
Qy 1975 CATAGAACCTCCAAACAAACATCAATTTTATTCACAGACTGACTGTAGTTAATTTTGTACA 2034

QY	605	GCCCGTGTGGA-CCGCCAGCCCCGGCTCCGCGCGCGCCCCCTTCACACC CGCGCC	664
Db	601	GCCC GTGTG G M C C C C S A G C G C G G C T C S G C G C G C C C C T C A C C C C G C G C G C C	660
QY	665	C A A G C C C A - G G G G C T C C T C G G G C T C A G T G G T T G T T G A C C T C C T G T A C T G G A G A G A C A T T A	723
Db	661	C A M G C G C A G G G G C T C T C G G G C T C A G T G T T G T T G A C C T C C T G T A C T G G A G A G A C A T T A	720
QY	724	A G A A G A C T G A G T G G T T G T T G F G C C A G C C T A T T C C T G C T G C T T C A T T G A C A G A T T C A	783
Db	721	A G A A G A C T G A G T G G T T G T T G G T G C C A G C C T A T T C C T G C T G C T T C A T T G A C A G A T T C A	780
QY	784	G C A T T C T G A G C G T P A A C A G C C T A C A T T G C C T T T G S C C C T G C T C T C T G T G A C C A T C A G C T T T A	843
Db	781	G C A T T C T G A G C G T P A A C A G C C T A C A T T G C C T T T G C C C T G C T C T C T G T G A C C A T C A G C T T T A	840
QY	844	G G A T A T A C A A G G T G T G A T C C A A G C T A T C A G A A A T C A G A T G A A G G C C A C C C A T T C A G G G	903
Db	841	G G A T A T A C A A G G T G T G A T C C A A G C T A T C A G A A A T C A G A T G A A G G C C A C C C A T T C A G G G	900
QY	904	C A T A T C T G A A	914
Db	901	C A T A T C T G A A	911
RESULT 9			
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LOCUS			
DEFINITION			
AL573494 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA			
clone CSOD1051YB11 3-PRIME, mRNA sequence.			
ACCESSION			
AL573494			
VERSION			
AL573494.3 GI:46246666			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 875)			
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
ON Feb 16, 2001 this sequence version replaced gi:31294840.			
COMMENT			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(df) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen. This sequence belongs to sequence cluster			
1423.r			
For more information about this cluster, see			
http://www.genoscope.cns.fr/cdna?s=CSOD1051CA06NP1&c=1423.r .			
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primer. Five prime end enriched, double-strand cDNA was			
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."			
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Query Match 38.4%; Score 861.2; DB 1; Length 875;			
Best Local Similarity 98.6%; Pred.No. 8.6e-179;			
Matches 863; Conservative 2; Mismatches 10; Indels 0; Gaps 0;			

Db	875	GTGTGTGACCTCCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTCTTTGGTGCCAGC	816
Qy	753	CTATTCCCTGCTCTTTCATTCAGACGATTTTCAGCATTTGTGAGCGTAACAGCCTACATTTGCC	812
Db	815	CTATTCCCTGCTCTTTCATTCAGCATTTTCAGCATTTGTGAGCGTAACAGCCTACATTTGCC	756
Qy	813	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGCTGTGATCCAAAGCTATC	872
Db	755	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGCTGTGATCCAAAGCTATC	696
Qy	873	CAGAAATCAGATGAAGAGCCACCATTCAGGCGATATCTGGAATCTGAAAGTTCCTATATCT	932
Db	695	CAGAAATCAGATGAAGAGCCACCATTCAGGCGATATCTGGAATCTGAAAGTTCCTATATCT	636
Qy	933	GAGGAGTTGGTTCAGAACTCAGATTAATCTGCTCTTGGCTCATGTGAACCTGCACGATAAAG	992
Db	635	GAGGAGTTGGTTCAGAACTCAGATTAATCTGCTCTTGGCTCATGTGAACCTGCACGATAAAG	576
Qy	993	GAACTCAGCGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG	1052
Db	575	GAACTCAGCGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG	516
Qy	1053	ATGTGGGTATTTACCTATGTTGGTGCCCTGTTTAAATGTCTGACACTACTGATTTTGGCT	1112
Db	515	ATGTGGGTATTTACCTATGTTGGTGCCCTGTTTAAATGTCTGACACTACTGATTTTGGCT	456
Qy	1113	CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGTAAGCGGCATCAGGCGACGATAGATCAT	1172
Db	455	CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGTAAGCGGCATCAGGCGACGATAGATCAT	396
Qy	1173	TATCTAGGACTTGCATAAAGAACTTAAAGATGCTATGGCTTAAATCCAAAGCAAAAATC	1232
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Qy	1233	CCTGGATTGAAGCGCAAAAGCTGAATGAAACGCCCAAAATAATTAGTAGGATTCATCTT	1292
Db	335	CCTGGATTGAAGCGCAAAAGCTGAATGAAACGCCCAAAATAATTAGTAGGATTCATCTT	276
Qy	1293	TAAAGGGATATTCATTTGATATACGGGGAGGGTCAGGGAAGAACGAACTTCAGCGTT	1352
Db	275	TAAAGGGATATTCATTTGATATACGGGGAGGGTCAGGGAAGAACGAACTTCAGCGTT	216
Qy	1353	GCAGTGCAGTTTCACAGATCGTTGTAGATCTTTATTTTATAGCCATGCACCTGTGTGAGG	1412
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Qy	1413	AAAAATTACCTGCTTGTGATGCTGCAATGTTTCATCATCTTAAGTATTTGAAGCTGCTATGT	1472
Db	155	AAAAATTACCTGCTTGTGATGCTGCAATGTTTCATCATCTTAAGTATTTGAAGCTGCTATGT	96
Qy	1473	ATGGATTTAAACCGTAATCATATCTTTTCTTATCTGAGGCACCTGGTGAATAAAAACC	1532
Db	95	ATGGATTTAAACCGTAATCATATCTTTTCTTATCTGAGGCACCTGGTGAATAAAAACC	36
Qy	1533	TGTATATTTTACTTTGTGTCAGATAGTCTTGCCGC	1567
Db	35	TGNANATNNNACTTGTGCGAGATAGTCTGCGCCG	1
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LOCUS	BM450461	1008 bp	mRNA linear EST 05-FEB-2002
DEFINITION	AGENCOURT_6394193 NIH_MGC_67	1008 bp	Hom sapiens cdna clone IMAGE:5494837
			5', mRNA sequence.
ACCESSION	BM450461		
VERSION	BM450461.1	GI:18499501	
KEYWORDS	EST.		
SOURCE	Hom sapiens (human)		
ORGANISM	Hom sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1008)		

AUTHORS		NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: Robert Straubeberg, Ph.D. Email: csapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12120 row: m column: 14 High quality sequence stop: 641.	
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		/clone_lib="NIH_MGC_67"	
		/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Library constructed by Life Technologies."	
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Qy	1279	TAGCAGTTTCATCTTTAAAGGGGATATTCATTTGATTTATACGGGGAGGGTCAGGGAAGAA	1338
Db	61	TAGCAGTTTCATCTTTAAAGGGGATATTCATTTGATTTATACGGGGAGGGTCAGGGAAGAA	120
Qy	1339	CGAACCTTGACGTTGCGAGTCAGTTTCACAGATCGTTGTTAGATCTTTATTTTAGCCAT	1398
Db	121	CGAACCTTGACGTTGCGAGTCAGTTTCACAGATCGTTGTTAGATCTTTATTTTAGCCAT	180
Qy	1399	GCATGTTGTGAGCAAAATTTACCTGCTTCACATGCGCATGTTTCATCATCTTAAGTATT	1458
Db	181	GCATGTTGTGAGCAAAATTTACCTGCTTCACATGCGCATGTTTCATCATCTTAAGTATT	240
Qy	1459	GTAAGCTGCTATGTATGATTTAAACCGTAAATCATATCTTTTCTATCTGAGGCACCTGG	1518
Db	241	GTAAGCTGCTATGTATGATTTAAACCGTAAATCATATCTTTTCTATCTGAGGCACCTGG	300
Qy	1519	TGGAATAAAAAACCTGTATATTTTACCTTTGTTGAGATGATGCTTCCCGCATCTTGGCAAG	1578
Db	301	TGGAATAAAAAACCTGTATATTTTACCTTTGTTGAGATGATGCTTCCCGCATCTTGGCAAG	360
Qy	1579	TTGCGAGATGCTGAGCTAG-AAAAAAGCCCTTTTCAGTTTGTGCACTG	1637
Db	361	TTGCGAGATGCTGAGCTAG-AAAAAAGCCCTTTTCAGTTTGTGCACTG	420
Qy	1638	TGTATGCTCCGTGTAGATTTGATGAGATTTTCTGAAATGAAATGTTTCTTTTAGACGAGAT	1697
Db	421	TGTATGCTCCGTGTAGATTTGATGAGATTTTCTGAAATGAAATGTTTCTTTTAGACGAGAT	480
Qy	1698	CATACCGGTAAAGCAGGAATGCAAAAGCTTCTTTCTGTTAGTGTCTAGGTGTTATGTTG	1757
Db	481	CATACCGGTAAAGCAGGAATGCAAAAGCTTCTTTCTGTTAGTGTCTAGGTGTTATGTTG	540
Qy	1758	ACTTTTACTGTTATTAATTTGCAATATAGTAATATAGATATATATATATATATATATAGTGT	1817
Db	541	ACTTTTACTGTTATTAATTTGCAATATAGTAATATAGTAATATATATATATATATATAGTGT	600


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RESULT 12
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LOCUS             clone IMAGE:6177832 5', mRNA sequence.
DEFINITION        AGENCOURT 8119868 Lupski dorsal root ganglion Homo sapiens cDNA
ACCESSION         BQ879359
VERSION           BQ879359.1 GI:22271367
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE         1. (bases 1 to 901)
                  NIH-MGC http://mgc.nci.nih.gov/.
                  National Institutes of Health, Mammalian Gene Collection (MGC)
                  Unpublished (1999)
                  Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-remail.nih.gov
                  Tissue Procurement: Dr. James R. Lupski
                  cDNA Library Preparation: Life Technologies, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Agencourt Bioscience Corporation
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LHAM13556 row: g column: 17
                  High quality sequence stop: 609.
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                   /lab_host="DH10B"
                   /clone_libs="Lupski dorsal root ganglion"
                   /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                   Not1; Site_2: SalI; cDNA made by oligo-dT priming.
                   Directionally cloned using the following adaptors:
                   5'-TCGACCCAGCGTCG-3' and
                   5'-GACATAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
                   1 kb for average insert length 1.7 kb. This is a primary
                   library, non-amplified. Library constructed by Life
                   Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                   College of Medicine) and is available through Life
                   Technologies."
ORIGIN
Query Match      37.4%; Score 837.2; DB 5; Length 901;
Best Local Similarity 97.7%; Pred. No. 1.7e-173;
Matches 881; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

Qy 802 CCTACATTGCGTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGA 861
Db 1 CCTACATTGCGTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAC-AGGGTGTGA 59
Qy 862 TCCAGCTATCAGAAATCAGATGAGGCCACCCATTGAGGCGATATCTGGAATCTGAAG 921
Db 60 TCCAGCTATCAGAAATCAGATGAGGCCACCCATTGAGGCGATATCTGGAATCTGAAG 119
Qy 922 TTGCTATATCTGAGGAGTTGGTTTCAGAGTAGTACAGTAATTCGTCTTGGTCAATGGAAC 981
Db 120 TTGCTATATCTGAGGAGTTGGTTTCAGAGTAGTACAGTAATTCGTCTTGGTCAATGGAAC 179
Qy 982 GCACGATAAAGGAATCAGGCGCCCTCTCTTTAGTTGATGATTTAGTTGATTTCTCTGAAGT 1041
Db 180 GCACGATAAAGGAATCAGGCGCCCTCTCTTTAGTTGATGATTTAGTTGATTTCTCTGAAGT 239
Qy 1042 TTGCAGTGTTCATGTTGGGTATTACCTATGTTGGTCCCTCTTTAAAGTGTGACACTAC 1101
Db 240 TTGCAGTGTTCATGTTGGGTATTTACCTATGTTGGTCCCTCTTTAAAGTGTGACACTAC 299

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Qy 1102 TGATTTGGCTCTCAATTTCACTTCTCAGTGTCTCTGTTATTATTATGAACGGCATCAGGCAC 1161
Db 300 TGAATTTGGCTCTCAATTTCACTTCTCAGTGTCTCTGTTATTATTATGAACGGCATCAGGCAC 359
Qy 1162 AGATAGATCATTTCTAGGACTTGCAGTTCGAAATAAGATGTTAAAGATGCTATGCTAAATCC 1221
Db 360 AGATAGATCATTTCTAGGACTTGCAGTTCGAAATAAGATGTTAAAGATGCTATGCTAAATCC 419
Qy 1222 AAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGAAACGCCCAAAATAATTTAGTAG 1281
Db 420 AAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGAAACGCCCAAAATAATTTAGTAG 479
Qy 1282 GAGTTTCATCTTTAAAGGGGATATTCACTTTGATTATACGGGGAGGGTTCAGGGAAGCA 1341
Db 480 GAGTTTCATCTTTAAAGGGGATATTCACTTTGATTATACGGGGAGGGTTCAGGGAAGCA 539
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Qy 1402 CTGTTGTGAGGAAAAATTTACCTGCTTGTGACGCGCATGTTTCATCATCTTAAAGTATTGTA 1461
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Qy 1462 AGCTGCTATGTATCGATTAAACCGTAAATCATATCTTTTCTATCTCAGGCACCTGGT-G 1520
Db 660 AGCTGCTATGTATCGATTAAACCGTAAATCATATCTTTTCTATCTCAGGCACCTGGTGG 719
Qy 1521 GAATAAAAAACCTGTATATTTTACTTTGTTGACATAGTCTTGGCGCATCTTGGCAAGTT 1580
Db 720 GAATAAAAAACCTGTATATTTTACTTTGTTGACATAGTCTTGGCGCATCTTGGCGAGTT 779
Qy 1581 GCAGAGATGTTGAGCTAGAAAAAAGCCCTTTTCAGTTTGTGCACTGTTGT 1640
Db 780 GCAGAGATGTTGAGCTAGAAAAAAGCCCTTTTCAGTTTGTGCACTGTTGT 839
Qy 1641 ATGTCGCTGTAGATTGATGACAGATTTTCTGAAATGAAATGTTT-GTTTAGCAGATCA 1699
Db 840 ATGTCGCTGTAGATTGATGACAGATTTTCTGAAATGAAATGTTTGGTTTAAACGAGATCC 899
Qy 1700 TA 1701
Db 900 TA 901

RESULT 13
CK232009          1164 bp  mRNA  linear  EST 09-DEC-2003
LOCUS             ILLUMIGEN MCQ 3196 Katze MMLP2 Macaca mulatta cDNA 5' similar to
DEFINITION        human RTN4 (Hs.436349), mRNA sequence.
ACCESSION         CK232009
VERSION           CK232009.1 GI:39638367
KEYWORDS          EST.
SOURCE            Macaca mulatta (rhesus monkey)
ORGANISM          Macaca mulatta
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                  Cercopithecinae; Macaca.
REFERENCE         1. (bases 1 to 1164)
                  Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magnus,C.L.
                  Large-scale Rhesus Macaque cDNA Sequencing
                  Unpublished (2003)
                  Contact: C. Magnus
                  Illumigen Biosciences Inc.
                  2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
                  Tel: 2063780400
                  Fax: 2063780408
                  Email: cmagnus@illumigen.com
                  Sequenced on 2003.11.25 797 Q20 bases. Assemblies in contig w/ 2
                  member(s). Contig contains 1 (0%) lib members.
                  PCR Primers
                  FORWARD: CCCTCACTAAAGGGAACAAAA

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Query Match		37.1%; Score 831; DB 7; Length 956;	
Best Local Similarity		95.3%; Pred. No. 4e-172;	
Matches		914; Conservative	0; Mismatches 30; Indels 15; Gaps 5;
QY	885	GAAGGCCACCATCTCAGGCGATATCTGGATCTGAAGTTGCTATATCTGAGGAGTTGGTT	944
DB	1	GAAGGCCACCATCTCAGGCGATATCTGGATCTGAAGTTGCTATATCTGAGGAGTTGGTT	60
QY	945	CAGAAGTACAGTAATCTCTGCTCTTGGTCATGTCAACTGCACGATAAAGAACTCAGGCGC	1004
DB	61	CAGAAGTACAGTAATCTCTGCTCTTGGTCATGTCAACTGCACGATAAAGAACTCAGGCGC	120
QY	1005	CTCTCTTAGTATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTGTGTTGGGTATTTT	1064
DB	121	CTCTCTTAGTATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTGTGTTGGGTATTTT	180
QY	1065	ACCTATGTTGGTGCCTTTGTTTAATGTCATCTGACACTACTGATTTTGGCTCTCATTTCACTC	1124
DB	181	ACCTATGTTGGTGCCTTTGTTTAATGTCATCTGACGCTACTGATTTTGGCTCTCATTTCACTC	240
QY	1125	TTCAAGTGTCTCTGTTTATATGACGCGCATCAGGCACAGATAGATCATTTCTAGGACTT	1184
DB	241	TTCAAGTGTCTCTGTTTATATGACGCGCATCAGGCACAGATAGATCATTTCTAGGACTT	300
QY	1185	GCAAAATGAAGATGTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATCCCTGGATTGAAG	1244
DB	301	GCAAAATGAAGATGTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATCCCTGGATTGAAG	360
QY	1245	CGCAAGCTGAATGAAACGCCCAAAATAATATAGTAGGAGTTTCATCTTTAAAGGGGATAT	1304
DB	361	CGCAAGCTGAATGAAACGCCCAAAATAATATAGTAGGAGTTTCATCTTTAAAGGGGATAT	420
QY	1305	TCATTTGATTTACGGGGAGGCTCAGGGAAGAACGAACTTGACGTTGCAGTGCAGTTT	1364
DB	421	TCATTTGATTTACGGGGAGGCTCAGGGAAGAACGAACTTGACATTCGAGTGCAGTTT	480
QY	1365	CACAGATCGTTGTAGATCTTTATTTTACCATGCACTGTTGTGAGGAGAAATTAACCTG	1424
DB	481	CACAGATCGTTGTAGATCTTTATTTTACCATGCACTGTTGTGAGGAGAAATTAACCTG	540
QY	1425	TCTTGACTGCCATGTGTTTCATCTTAAGTATGTAAGCTGCTATGTATGGATTTAAAC	1484
DB	541	TCTTGACTGCCATGTGTTTCATCTTAAGTATGTAAGCTGCTATGTATGGATTTAAAC	599
QY	1485	CGTAATCATATCTTTTCCATCTCTGAGGCACTGGTGGATATAAAACCTGTATATTTTAC	1544
DB	600	CGTAATCATATCTTTTCCATCTCTGAGGCACTGGTGGATATAAAACCTGTATATTTTAC	659
QY	1545	TTTGTGTCAGATAGTCTTGGCGCATCTTGGCAAGTTGTCAGAGATGTTGGAGCTAGAAAAA	1604
DB	660	TTTGTGTCAGATAGTCTTGGCGCATCTTGGCAAGTTGTCAGAGATGTTGGAGTTAG----	714
QY	1605	AAAAAAGAGCCCTTTTTCAGTTTGTGCACTGTGTATGTTCCGTGTAGATTCATGCAGA	1664
DB	715	----AAAAAAGAGCCCTTTTTCAGTTTGTGCACTGTGTATGTTCCGTGTAGATTCATGCAGA	771
QY	1665	TTTTCTGAAATGAAATGTTTGTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAG	1724
DB	772	TTTTCTGAAATGAAATGTTTGTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAT	827
QY	1725	CTTGCTTTTCTGGTATGTTCTAGGTGTATGTCAC-TTTTTACGTGTATATTAATTCGCCAA	1783
DB	828	CTTGCTTTTCTGGTATGTTCTAGGTGTATGTCACTTTTTACGTGTATATTAATTCGCCAA	887
QY	1784	TATAAGTAAATATAGATTATATATATATATATATAGTGTGTTTACAAAGCTTAGACCTTTACCTT	1841
DB	888	TATAAGTAAATATAGATTATATATATATATATATAGTGTGTTTACAAAGCTTTAAACCTTTACCT	946
RESULT 15		1031 bp	mRNA
CN647521			EST 13-MAY-2004
LOCUS			

RESULT 15
CN647521


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Qy 1052 GATGTGGGTATTTACCTATGTTGGTGCCTTGTGCTTTAAATGGTCTGACACTACTGATTTTGGC 1111
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
488 GATGTGGGTATTTACCTATGTTGGTGCCTTGTGCTTTAAATGGTCTGACACTACTGATTTTGGC 547
Qy 1112 TCTCATTTTCACTCTTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCA 1171
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
548 TCTCATTTTCACTCTTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCA 607
Qy 1172 TTATCTAGGACTTGCAAATAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAAT 1231
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
608 TTATCTAGGACTTGCAAATAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCGAAAAT 667
Qy 1232 CCCTGGATTTGAAGCGCAAGCTGAATGAAGCGCCAAAATAATTAGTAGAGTTCACTCT 1291
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
668 CCCTGGATTTGAAGCGCAAGCTGAATGAAGCAACCCAAAATAATTTACTAGGAGTTCACTCT 727
Qy 1292 TTAAGGGGATATTTCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAACCTTGACGT 1351
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728 TTAAGGGGGTATTTCATTTGAGTATATGGGGGAGGGTCAGGGAAGAACGAACCTTGACTT 787
Qy 1352 TGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTTATTTTGTAGCCATGCACTGTTGTGAG 1411
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788 TGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTTATTTTACCATGCCCTGTTGTGAG 847
Qy 1412 GAAAAATTTACCTGTCTTGACTGCGCATGTGTTTCATCATCTTAAAGTATTTGTAGCTGCTATG 1471
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848 GAAAAATTTACCTGTCTTGACTGCGCATGTGTTTCCTCTCTC-TAAAGTATTTGTAACTGCTATG 906
Qy 1472 TATCGATTTAAACCGTAATCATATCTTTTTCCTATCTGAGGCACCTGGTGGAAATAAAAAC 1531
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
907 AATCGATTTAAACCGTAATCATATCTTTTTCCTATCTGAGCCCTCGGGGGAAATAAAAAC 966
Qy 1532 CTGTATATTTTACTTTTGTGAGATAGTCTTGCGGCAT-CTTGGCAAAGTTGCAGAGATGG 1590
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
967 CTGAATATTTTACTTTTGTGAGGTAACTTGTCTGCCTCTGCGCAAGTTGCCAAAAGG 1026
Qy 1591 TGGA 1594
Db |||
1027 GGGA 1030
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Search completed: August 1, 2005, 20:03:47
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